

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problems Mailbox.**

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Bosch, Hendrick J.
Stiekema, Willem J.
- (ii) TITLE OF INVENTION: Hybrid Toxin
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Novartis Corporation
(B) STREET: 3054 Cornwallis Road
(C) CITY: Research Triangle Park
(D) STATE: NC
(E) COUNTRY: USA
(F) ZIP: 27709
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/602,737
(B) FILING DATE: 21-FEB-1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Meigs, J. Timothy
(B) REGISTRATION NUMBER: 38,241
(C) REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 919-541-8587
(B) TELEFAX: 919-541-8689

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3567 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacillus thuringiensis*
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..3567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATG GAG GAA AAT AAT CAA AAT CAA TGC ATA CCT TAC AAT TGT TTA AGT	48
Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser	
1 5 10 15	
AAT CCT GAA GAA GTA CTT TTG GAT GGA GAA CGG ATA TCA ACT GGT AAT	96
Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn	
20 25 30	
TCA TCA ATT GAT ATT TCT CTG TCA CTT GTT CAG TTT CTG GTA TCT AAC	144
Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn	
35 40 45	
TTT GTA CCA GGG GGA GGA TTT TTA GTT GGA TTA ATA GAT TTT GTA TGG	192
Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp	
50 55 60	
GGA ATA GTT GGC CCT TCT CAA TGG GAT GCA TTT CTA GTA CAA ATT GAA	240
Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu	
65 70 75 80	
CAA TTA ATT AAT GAA AGA ATA GCT GAA TTT GCT AGG AAT GCT GCT ATT	288
Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile	
85 90 95	
GCT AAT TTA GAA GGA TTA GGA AAC AAT TTC AAT ATA TAT GTG GAA GCA	336
Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala	
100 105 110	
TTT AAA GAA TGG GAA GAA GAT CCT AAT AAT CCA GAA ACC AGG ACC AGA	384
Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Glu Thr Arg Thr Arg	
115 120 125	
GTA ATT GAT CGC TTT CGT ATA CTT GAT GGG CTA CTT GAA AGG GAC ATT	432
Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Glu Arg Asp Ile	
130 135 140	
CCT TCG TTT CGA ATT TCT GGA TTT GAA GTA CCC CTT TTA TCC GTT TAT	480

Pro Ser Phe Arg Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr
145 150 155 160

GCT CAA GCG GCC AAT CTG CAT CTA GCT ATA TTA AGA GAT TCT GTA ATT 528
Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile
165 170 175

TTT GGA GAA AGA TGG GGA TTG ACA ACG ATA AAT GTC AAT GAA AAC TAT 576
Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr
180 185 190

AAT AGA CTA ATT AGG CAT ATT GAT GAA TAT GCT GAT CAC TGT GCA AAT 624
Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn
195 200 205

ACG TAT AAT CGG GGA TTA AAT AAT TTA CCG AAA TCT ACG TAT CAA GAT 672
Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp
210 215 220

TGG ATA ACA TAT AAT CGA TTA CGG AGA GAC TTA ACA TTG ACT GTA TTA 720
Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu
225 230 235 240

GAT ATC GCC GCT TTC TTT CCA AAC TAT GAC AAT AGG AGA TAT CCA ATT 768
Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile
245 250 255

CAG CCA GTT GGT CAA CTA ACA AGG GAA GTT TAT ACG GAC CCA TTA ATT 816
Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile
260 265 270

AAT TTT AAT CCA CAG TTA CAG TCT GTA GCT CAA TTA CCT ACT TTT AAC 864
Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn
275 280 285

GTT ATG GAG AGC AGC GCA ATT AGA AAT CCT CAT TTA TTT GAT ATA TTG 912
Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu
290 295 300

AAT AAT CTT ACA ATC TTT ACG GAT TGG TTT AGT GTT GGA CGC AAT TTT 960
Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe
305 310 315 320

TAT TGG GGA GGA CAT CGA GTA ATA TCT AGC CTT ATA GGA GGT GGT AAC 1008
Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Gly Asn
325 330 335

ATA ACA TCT CCT ATA TAT GGA AGA GAG GCG AAC CAG GAG CCT CCA AGA 1056
Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg
340 345 350

TCC TTT ACT TTT AAT GGA CCG GTA TTT AGG ACT TTA TCA AAT CCT ACT 1104
Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr

355	360	365	
TTA CGA TTA TTA CAG CAA CCT TGG CCA GCG CCA CCA TTT AAT TTA CGT			1152
Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg			
370	375	380	
GGT GTT GAA GGA GTA GAA TTT TCT ACA CCT ACA AAT AGC TTT ACG TAT			1200
Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr			
385	390	395	400
CGA GGA AGA GGT ACG GTT GAT TCT TTA ACT GAA TTA CCG CCT GAG GAT			1248
Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp			
405	410	415	
AAT AGT GTG CCA CCT CGC GAA GGA TAT AGT CAT CGT TTA TGT CAT GCA			1296
Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala			
420	425	430	
ACT TTT GTT CAA AGA TCT GGA ACA CCT TTT TTA ACA ACT GGT GTA GTA			1344
Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val			
435	440	445	
TTT TCT TGG ACG CAT CGT AGT GCA ACT CTT ACA AAT ACA ATT GAT CCA			1392
Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro			
450	455	460	
GAG AGA ATT AAT CAA ATA CCT TTA GTG AAA GGA TTT AGA GTT TGG GGG			1440
Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly			
465	470	475	480
GGC ACC TCT GTC ATT ACA GGA CCA GGA TTT ACA GGA GGG GAT ATC CTT			1488
Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu			
485	490	495	
CGA AGA AAT ACC TTT GGT GAT TTT GTA TCT CTA CAA GTC AAT ATT AAT			1536
Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn			
500	505	510	
TCA CCA ATT ACC CAA AGA TAC CGT TTA AGA TTT CGT TAC GCT TCC AGT			1584
Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser			
515	520	525	
AGG GAT GCA CGA GTT ATA GTA TTA ACA GGA GCG GCA TCC ACA GGA GTG			1632
Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val			
530	535	540	
GGA GGC CAA GTT AGT GTA AAT ATG CCT CTT CAG AAA ACT ATG GAA ATA			1680
Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile			
545	550	555	560
GGG GAG AAC TTA ACA TCT AGA ACA TTT AGA TAT ACC GAT TTT AGT AAT			1728
Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn			
565	570	575	

CCT TTT TCA TTT AGA GCT AAT CCA GAT ATA ATT GGG ATA AGT GAA CAA	1776
Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln	
580 585 590	
CCT CTA TTT GGT GCA GGT TCT ATT AGT AGC GGT GAA CTT TAT ATA GAT	1824
Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp	
595 600 605	
AAA ATT GAA ATT ATT CTA GCA GAT GCA ACA TTT GAA GCA GAA TCT GAT	1872
Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp	
610 615 620	
TTA GAA AGA GCA CAA AAG GCG GTG AAT GCC CTG TTT ACT TCT TCC AAT	1920
Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn	
625 630 635 640	
CAA ATC GGG TTA AAA ACC GAT GTG ACG GAT TAT CAT ATT GAT CAA GTA	1968
Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val	
645 650 655	
TCC AAT TTA GTG GAT TGT TTA TCA GAT GAA TTT TGT CTG GAT GAA AAG	2016
Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys	
660 665 670	
CGA GAA TTG TCC GAG AAA GTC AAA CAT GCG AAG CGA CTC AGT GAT GAG	2064
Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu	
675 680 685	
CGG AAT TTA CTT CAA GAT CCA AAC TTC AGA GGG ATC AAT AGA CAA CCA	2112
Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro	
690 695 700	
GAC CGT GGC TGG AGA GGA AGT ACA GAT ATT ACC ATC CAA GGA GGA GAT	2160
Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp	
705 710 715 720	
GAC GTA TTC AAA GAG AAT TAC GTC ACA CTA CCG GGT ACC GTT GAT GAG	2208
Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu	
725 730 735	
TGC TAT CCA ACG TAT TTA TAT CAG AAA ATA GAT GAG TCG AAA TTA AAA	2256
Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys	
740 745 750	
GCT TAT ACC CGT TAT GAA TTA AGA GGG TAT ATC GAA GAT AGT CAA GAC	2304
Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp	
755 760 765	
TTA GAA ATC TAT TTG ATC CGT TAC AAT GCA AAA CAC GAA ATA GTA AAT	2352
Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn	
770 775 780	

GTG CCA GGC ACG GGT TCC TTA TGG CCG CTT TCA GCC CAA AGT CCA ATC 2400
 Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile
 785 790 795 800

GGA AAG TGT GGA GAA CCG AAT CGA TGC GCG CCA CAC CTT GAA TGG AAT 2448
 Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn
 805 810 815

CCT GAT CTA GAT TGT TCC TGC AGA GAC GGG GAA AAA TGT GCA CAT CAT 2496
 Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His
 820 825 830

TCC CAT CAT TTC ACC TTG GAT ATT GAT GTT GGA TGT ACA GAC TTA AAT 2544
 Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn
 835 840 845

GAG GAC TTA GGT GTA TGG GTG ATA TTC AAG ATT AAG ACG CAA GAT GGC 2592
 Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly
 850 855 860

CAT GCA AGA CTA GGG AAT CTA GAG TTT CTC GAA GAG AAA CCA TTA TTA 2640
 His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu
 865 870 875 880

GGG GAA GCA CTA GCT CGT GTG AAA AGA GCG GAG AAG AAG TGG AGA GAC 2688
 Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp
 885 890 895

AAA CGA GAG AAA CTG CAG TTG GAA ACA AAT ATT GTT TAT AAA GAG GCA 2736
 Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala
 900 905 910

AAA GAA TCT GTA GAT GCT TTA TTT GTA AAC TCT CAA TAT GAT AGA TTA 2784
 Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu
 915 920 925

CAA GTG GAT ACG AAC ATC GCG ATG ATT CAT GCG GCA GAT AAA CGC GTT 2832
 Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val
 930 935 940

CAT AGA ATC CGG GAA GCG TAT CTG CCA GAG TTG TCT GTG ATT CCA GGT 2880
 His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly
 945 950 955 960

GTC AAT GCG GCC ATT TTC GAA GAA TTA GAG GGA CGT ATT TTT ACA GCG 2928
 Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala
 965 970 975

TAT TCC TTA TAT GAT GCG AGA AAT GTC ATT AAA AAT GGC GAT TTC AAT 2976
 Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn
 980 985 990

AAT GGC TTA TTA TGC TGG AAC GTG AAA GGT CAT GTA GAT GTA GAA GAG 3024

002260-05939300

Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu
 995 1000 1005

CAA AAC AAC CAC CGT TCG GTC CTT GTT ATC CCA GAA TGG GAG GCA GAA 3072
 Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu
 1010 1015 1020

GTG TCA CAA GAG GTT CGT GTC TGT CCA GGT CGT GGC TAT ATC CTT CGT 3120
 Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg
 1025 1030 1035 1040

GTC ACA GCA TAT AAA GAG GGA TAT GGA GAG GGC TGC GTA ACG ATC CAT 3168
 Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His
 1045 1050 1055

GAG ATC GAA GAC AAT ACA GAC GAA CTG AAA TTC AGC AAC TGT GTA GAA 3216
 Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu
 1060 1065 1070

GAG GAA GTA TAT CCA AAC AAC ACA GTA ACG TGT AAT AAT TAT ACT GGG 3264
 Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly
 1075 1080 1085

ACT CAA GAA GAA TAT GAG GGT ACG TAC ACT TCT CGT AAT CAA GGA TAT 3312
 Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr
 1090 1095 1100

GAC GAA GCC TAT GGT AAT AAC CCT TCC GTA CCA GCT GAT TAC GCT TCA 3360
 Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser
 1105 1110 1115 1120

GTC TAT GAA GAA AAA TCG TAT ACA GAT GGA CGA AGA GAG AAT CCT TGT 3408
 Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys
 1125 1130 1135

GAA TCT AAC AGA GGC TAT GGG GAT TAC ACA CCA CTA CCG GCT GGT TAT 3456
 Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
 1140 1145 1150

GTA ACA AAG GAT TTA GAG TAC TTC CCA GAG ACC GAT AAG GTA TGG ATT 3504
 Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile
 1155 1160 1165

GAG ATC GGA GAA ACA GAA GGA ACA TTC ATC GTG GAT AGC GTG GAA TTA 3552
 Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu
 1170 1175 1180

CTC CTT ATG GAG GAA 3567
 Leu Leu Met Glu Glu
 1185

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1189 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser
 1 5 10 15

Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn
 20 25 30

Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn
 35 40 45

Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp
 50 55 60

Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu
 65 70 75 80

Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile
 85 90 95

Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala
 100 105 110

Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Glu Thr Arg Thr Arg
 115 120 125

Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile
 130 135 140

Pro Ser Phe Arg Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr
 145 150 155 160

Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile
 165 170 175

Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr
 180 185 190

Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn
 195 200 205

Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp
 210 215 220

Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu

225 230 235 240
 Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile
 245 250 255
 Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile
 260 265 270
 Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn
 275 280 285
 Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu
 290 295 300
 Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe
 305 310 315 320
 Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Gly Asn
 325 330 335
 Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg
 340 345 350
 Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr
 355 360 365
 Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg
 370 375 380
 Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr
 385 390 395 400
 Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp
 405 410 415
 Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala
 420 425 430
 Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val
 435 440 445
 Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro
 450 455 460
 Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly
 465 470 475 480
 Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu
 485 490 495
 Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn
 500 505 510

Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser
 515 520 525
 Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val
 530 535 540
 Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile
 545 550 555 560
 Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn
 565 570 575
 Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln
 580 585 590
 Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp
 595 600 605
 Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp
 610 615 620
 Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn
 625 630 635 640
 Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val
 645 650 655
 Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys
 660 665 670
 Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu
 675 680 685
 Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro
 690 695 700
 Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp
 705 710 715 720
 Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu
 725 730 735
 Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys
 740 745 750
 Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp
 755 760 765
 Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn
 770 775 780
 Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile
 785 790 795 800

000000-03989900

Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn
 805 810 815
 Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His
 820 825 830
 Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn
 835 840 845
 Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly
 850 855 860
 His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu
 865 870 875 880
 Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp
 885 890 895
 Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala
 900 905 910
 Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu
 915 920 925
 Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val
 930 935 940
 His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly
 945 950 955 960
 Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala
 965 970 975
 Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn
 980 985 990
 Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu
 995 1000 1005
 Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu
 1010 1015 1020
 Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg
 1025 1030 1035 1040
 Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His
 1045 1050 1055
 Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu
 1060 1065 1070
 Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly

1075 1080 1085

Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr
 1090 1095 1100

Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser
 1105 1110 1115 1120

Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys
 1125 1130 1135

Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
 1140 1145 1150

Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile
 1155 1160 1165

Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu
 1170 1175 1180

Leu Leu Met Glu Glu
 1185

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATG GAG ATA GTG AAT AAT CAG AAT CAA TGC GTG CCT TAT AAT TGT TTA	48
Met Glu Ile Val Asn Asn Gln Asn Gln Cys Val Pro Tyr Asn Cys Leu	
1 5 10 15	
AAT AAT CCT GAA AAT GAG ATA TTA GAT ATT GAA AGG TCA AAT AGT ACT	96
Asn Asn Pro Glu Asn Glu Ile Leu Asp Ile Glu Arg Ser Asn Ser Thr	

20	25	30	
GTA GCA ACA AAC ATC GCC TTG GAG ATT AGT CGT CTG CTC GCT TCC GCA			144
Val Ala Thr Asn Ile Ala Leu Glu Ile Ser Arg Leu Leu Ala Ser Ala			
35	40	45	
ACT CCA ATA GGG GGG ATT TTA TTA GGA TTG TTT GAT GCA ATA TGG GGG			192
Thr Pro Ile Gly Gly Ile Leu Leu Gly Leu Phe Asp Ala Ile Trp Gly			
50	55	60	
TCT ATA GGC CCT TCA CAA TGG GAT TTA TTT TTA GAG CAA ATT GAG CTA			240
Ser Ile Gly Pro Ser Gln Trp Asp Leu Phe Leu Glu Gln Ile Glu Leu			
65	70	75	80
TTG ATT GAC CAA AAA ATA GAG GAA TTC GCT AGA AAC CAG GCA ATT TCT			288
Leu Ile Asp Gln Lys Ile Glu Glu Phe Ala Arg Asn Gln Ala Ile Ser			
85	90	95	
AGA TTG GAA GGG ATA AGC AGT CTG TAC GGA ATT TAT ACA GAA GCT TTT			336
Arg Leu Glu Gly Ile Ser Ser Leu Tyr Gly Ile Tyr Thr Glu Ala Phe			
100	105	110	
AGA GAG TGG GAA GCA GAT CCT ACT AAT CCA GCA TTA AAA GAA GAG ATG			384
Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Lys Glu Glu Met			
115	120	125	
CGT ACT CAA TTT AAT GAC ATG AAC AGT ATT CTT GTA ACA GCT ATT CCT			432
Arg Thr Gln Phe Asn Asp Met Asn Ser Ile Leu Val Thr Ala Ile Pro			
130	135	140	
CTT TTT TCA GTT CAA AAT TAT CAA GTC CCA TTT TTA TCA GTA TAT GTT			480
Leu Phe Ser Val Gln Asn Tyr Gln Val Pro Phe Leu Ser Val Tyr Val			
145	150	155	160
CAA GCT GCA AAT TTA CAT TTA TCG GTT TTG AGA GAT GTT TCA GTG TTT			528
Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser Val Phe			
165	170	175	
GGG CAG GCT TGG GGA TTT GAT ATA GCA ACA ATA AAT AGT CGT TAT AAT			576
Gly Gln Ala Trp Gly Phe Asp Ile Ala Thr Ile Asn Ser Arg Tyr Asn			
180	185	190	
GAT CTG ACT AGA CTT ATT CCT ATA TAT ACA GAT TAT GCT GTA CGC TGG			624
Asp Leu Thr Arg Leu Ile Pro Ile Tyr Thr Asp Tyr Ala Val Arg Trp			
195	200	205	
TAC AAT ACG GGA TTA GAT CGC TTA CCA CGA ACT GGT GGG CTG CGA AAC			672
Tyr Asn Thr Gly Leu Asp Arg Leu Pro Arg Thr Gly Gly Leu Arg Asn			
210	215	220	
TGG GCA AGA TTT AAT CAG TTT AGA AGA GAG TTA ACA ATA TCA GTA TTA			720
Trp Ala Arg Phe Asn Gln Phe Arg Arg Glu Leu Thr Ile Ser Val Leu			
225	230	235	240

GAT ATT ATT TCT TTT TTC AGA AAT TAC GAT TCT AGA TTA TAT CCA ATT Asp Ile Ile Ser Phe Phe Arg Asn Tyr Asp Ser Arg Leu Tyr Pro Ile 245 250 255	768
CCA ACA AGC TCC CAA TTA ACG CGG GAA GTA TAT ACA GAT CCG GTA ATT Pro Thr Ser Ser Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Val Ile 260 265 270	816
AAT ATA ACT GAC TAT AGA GTT GGC CCC AGC TTC GAG AAT ATT GAG AAC Asn Ile Thr Asp Tyr Arg Val Gly Pro Ser Phe Glu Asn Ile Glu Asn 275 280 285	864
TCA GCC ATT AGA AGC CCC CAC CTT ATG GAC TTC TTA AAT AAT TTG ACC Ser Ala Ile Arg Ser Pro His Leu Met Asp Phe Leu Asn Asn Leu Thr 290 295 300	912
ATT GAT ACG GAT TTG ATT AGA GGT GTT CAC TAT TGG GCA GGG CAT CGT Ile Asp Thr Asp Leu Ile Arg Gly Val His Tyr Trp Ala Gly His Arg 305 310 315 320	960
GTA ACT TCT CAT TTT ACA GGT AGT TCT CAA GTG ATA ACA ACC CCT CAA Val Thr Ser His Phe Thr Gly Ser Ser Gln Val Ile Thr Thr Pro Gln 325 330 335	1008
TAT GGG ATA ACC GCA AAT GCG GAA CCA AGA CGA ACT ATT GCT CCT AGT Tyr Gly Ile Thr Ala Asn Ala Glu Pro Arg Arg Thr Ile Ala Pro Ser 340 345 350	1056
ACT TTT CCA GGT CTT AAC CTA TTT TAT AGA ACA TTA TCA AAT CCT TTC Thr Phe Pro Gly Leu Asn Leu Phe Tyr Arg Thr Leu Ser Asn Pro Phe 355 360 365	1104
TTC CGA AGA TCA GAA AAT ATT ACT CCT ACC TTA GGG ATA AAT GTA GTA Phe Arg Arg Ser Glu Asn Ile Thr Pro Thr Leu Gly Ile Asn Val Val 370 375 380	1152
CAG GGA GTA GGG TTC ATT CAA CCA AAT AAT GCT GAA GTT CTA TAT AGA Gln Gly Val Gly Phe Ile Gln Pro Asn Asn Ala Glu Val Leu Tyr Arg 385 390 395 400	1200
AGT AGG GGG ACA GTA GAT TCT CTT AAT GAG TTA CCA ATT GAT GGT GAG Ser Arg Gly Thr Val Asp Ser Leu Asn Glu Leu Pro Ile Asp Gly Glu 405 410 415	1248
AAT TCA TTA GTT GGA TAT AGT CAT CGA TTA AGT CAT GTT ACA CTA ACC Asn Ser Leu Val Gly Tyr Ser His Arg Leu Ser His Val Thr Leu Thr 420 425 430	1296
AGG TCG TTA TAT AAT ACT AAT ATA ACT AGC CTG CCA ACA TTT GTT TGG Arg Ser Leu Tyr Asn Thr Asn Ile Thr Ser Leu Pro Thr Phe Val Trp 435 440 445	1344

ACA CAT CAC AGT GCT ACT AAT ACA AAT ACA ATT AAT CCA GAT ATT ATT 1392
 Thr His His Ser Ala Thr Asn Thr Asn Thr Ile Asn Pro Asp Ile Ile
 450 455 460

ACA CAA ATA CCT TTA GTG AAA GGA TTT AGA CTT GGT GGT GGC ACC TCT 1440
 Thr Gln Ile Pro Leu Val Lys Gly Phe Arg Leu Gly Gly Gly Thr Ser
 465 470 475 480

GTC ATT AAA GGA CCA GGA TTT ACA GGA GGG GAT ATC CTT CGA AGA AAT 1488
 Val Ile Lys Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Asn
 485 490 495

ACC ATT GGT GAG TTT GTG TCT TTA CAA GTC AAT ATT AAC TCA CCA ATT 1536
 Thr Ile Gly Glu Phe Val Ser Leu Gln Val Asn Ile Asn Ser Pro Ile
 500 505 510

ACC CAA AGA TAC CGT TTA AGA TTT CGT TAT GCT TCC AGT AGG GAT GCA 1584
 Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser Arg Asp Ala
 515 520 525

CGA ATT ACT GTA GCG ATA GGA GGA CAA ATT AGA GTA GAT ATG ACC CTT 1632
 Arg Ile Thr Val Ala Ile Gly Gly Gln Ile Arg Val Asp Met Thr Leu
 530 535 540

GAA AAA ACC ATG GAA ATT GGG GAG AGC TTA ACA TCT AGA ACA TTT AGC 1680
 Glu Lys Thr Met Glu Ile Gly Glu Ser Leu Thr Ser Arg Thr Phe Ser
 545 550 555 560

TAT ACC AAT TTT AGT AAT CCT TTT TCA TTT AGG GCT AAT CCA GAT ATA 1728
 Tyr Thr Asn Phe Ser Asn Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile
 565 570 575

ATT AGA ATA GCT GAA GAA CTT CCT ATT CGT GGT GGT GAG CTT TAT ATA 1776
 Ile Arg Ile Ala Glu Glu Leu Pro Ile Arg Gly Gly Glu Leu Tyr Ile
 580 585 590

GAT AAA ATT GAA CTT ATT CTA GCA GAT GCA ACA TTT GAA GAA GAA TAT 1824
 Asp Lys Ile Glu Leu Ile Leu Ala Asp Ala Thr Phe Glu Glu Glu Tyr
 595 600 605

GAT TTG GAA AGA GCA CAG AAG GCG GTG AAT GCC CTG TTT ACT TCT ACA 1872
 Asp Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Thr
 610 615 620

AAT CAA CTA GGG CTA AAA ACA GAT GTG ACG GAT TAT CAT ATT GAT CAA 1920
 Asn Gln Leu Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln
 625 630 635 640

GTT TCC AAT TTA GTT GAG TGT TTA TCG GAT GAA TTT TGT CTG GAT GAA 1968
 Val Ser Asn Leu Val Glu Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu
 645 650 655

AAG AGA GAA TTA TCC GAG AAA GTC AAA CAT GCG AAG CGA CTC AGT GAT 2016

Lys Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp
 660 665 670

GAA CGG AAT TTA CTT CAA GAT CCA AAC TTC AGA GGG ATC AAT AGG CAA 2064
 Glu Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln
 675 680 685

CCA GAC CGT GGC TGG AGA GGA AGC ACG GAT ATT ACT ATC CAA GGT GGA 2112
 Pro Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly
 690 695 700

GAT GAC GTA TTC AAA GAG AAT TAC GTC ACA TTA CCG GGT ACC TTT GAT 2160
 Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Phe Asp
 705 710 715 720

GAG TGC TAT CCA ACG TAT TTA TAT CAA AAA ATA GAT GAG TCG AAG TTA 2208
 Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu
 725 730 735

AAA GCT TAT ACC CGC TAT GAA TTA AGA GGG TAT ATC GAG GAT AGT CAA 2256
 Lys Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln
 740 745 750

GAC TTA GAA ATC TAT TTA ATT CGC TAC AAT GCA AAA CAC GAG ACA GTA 2304
 Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Val
 755 760 765

AAC GTG CCA GGT ACG GGT TCC TTA TGG CCG CTT TCA GCC CAA AGT CCA 2352
 Asn Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro
 770 775 780

ATC GGA AAG TGT GGA GAA CCG AAT CGA TGC GCG CCA CAC CTT GAA TGG 2400
 Ile Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp
 785 790 795 800

AAT CCT AAT CTA GAT TGC TCC TGC AGA GAC GGG GAA AAA TGT GCC CAT 2448
 Asn Pro Asn Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His
 805 810 815

CAT TCC CAT CAT TTC TCC TTG GAC ATT GAT GTT GGA TGT ACA GAC TTA 2496
 His Ser His His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu
 820 825 830

AAT GAG GAC TTA GGT GTA TGG GTG ATA TTC AAG ATT AAG ACA CAA GAT 2544
 Asn Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp
 835 840 845

GGC TAT GCA AGA CTA GGA AAT CTA GAG TTT CTC GAA GAG AAC CCA CTA 2592
 Gly Tyr Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Asn Pro Leu
 850 855 860

TTA GGG GAA GCA CTA GCT CGT GTG AAA AGA GCG GAG AAA AAA TGG AGA 2640
 Leu Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg

865	870	875	880	
GAC AAA TGC GAA AAA TTG GAA TGG GAA ACA AAT ATT GTT TAT AAA GAG				2688
Asp Lys Cys Glu Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr Lys Glu	885	890	895	
GCA AAA GAA TCT GTA GAT GCT TTA TTT GTA AAC TCT CAA TAT GAT AGA				2736
Ala Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg	900	905	910	
TTA CAA GCG GAT ACG AAT ATC GCG ATG ATT CAT GCG GCA GAT AAA CGC				2784
Leu Gln Ala Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg	915	920	925	
GTT CAT AGC ATT CGA GAA GCG TAT CTG CCA GAG CTG TCT GTG ATT CCG				2832
Val His Ser Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro	930	935	940	
GGT GTC AAT GCG GCT ATT TTT GAA GAA TTA GAA GGG CGT ATT TTC ACT				2880
Gly Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr	945	950	955	960
GCA TTC TCC CTA TAT GAT GCG AGA AAT GTC ATT AAA AAT GGC GAT TTC				2928
Ala Phe Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe	965	970	975	
AAT AAT GGC TTA TCA TGC TGG AAC GTG AAA GGG CAT GTA GAT GTA GAA				2976
Asn Asn Gly Leu Ser Cys Trp Asn Val Lys Gly His Val Asp Val Glu	980	985	990	
GAA CAG AAC AAC CAT CGT TCG GTC CTT GTT GTT CCA GAA TGG GAA GCA				3024
Glu Gln Asn Asn His Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala	995	1000	1005	
GAA GTG TCA CAA GAA GTT CGT GTT TGT CCG GGT CGT GGC TAT ATC CTT				3072
Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu	1010	1015	1020	
CGT GTT ACA GCG TAC AAA GAG GGA TAT GGA GAG GGC TGT GTA ACG ATT				3120
Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile	1025	1030	1035	1040
CAT GAG ATC GAA GAC AAT ACA GAC GAA CTG AAA TTC AGC AAC TGT GTA				3168
His Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val	1045	1050	1055	
GAA GAG GAA GTA TAT CCA AAC AAC ACG GTA ACG TGT AAT AAT TAT ACT				3216
Glu Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr	1060	1065	1070	
GCG ACT CAA GAA GAA CAT GAG GGT ACG TAC ACT TCC CGT AAT CGA GGA				3264
Ala Thr Gln Glu Glu His Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly	1075	1080	1085	

TAT GAC GAA GCC TAT GAA AGC AAT TCT TCT GTA CAT GCG TCA GTC TAT 3312
 Tyr Asp Glu Ala Tyr Glu Ser Asn Ser Ser Val His Ala Ser Val Tyr
 1090 1095 1100
 GAA GAA AAA TCG TAT ACA GAT AGA CGA AGA GAG AAT CCT TGT GAA TCT 3360
 Glu Glu Lys Ser Tyr Thr Asp Arg Arg Arg Glu Asn Pro Cys Glu Ser
 1105 1110 1115 1120
 AAC AGA GGA TAT GGG GAT TAC ACA CCA CTA CCA GCT GGC TAT GTG ACA 3408
 Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr
 1125 1130 1135
 AAA GAA TTA GAG TAC TTC CCA GAA ACC GAT AAG GTA TGG ATT GAG ATC 3456
 Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile
 1140 1145 1150
 GGA GAA ACG GAA GGA ACA TTC ATC GTG GAC AGC GTG GAA TTA CTT CTT 3504
 Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu Leu
 1155 1160 1165
 ATG GAG GAA 3513
 Met Glu Glu
 1170

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1171 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Glu Ile Val Asn Asn Gln Asn Gln Cys Val Pro Tyr Asn Cys Leu
 1 5 10 15
 Asn Asn Pro Glu Asn Glu Ile Leu Asp Ile Glu Arg Ser Asn Ser Thr
 20 25 30
 Val Ala Thr Asn Ile Ala Leu Glu Ile Ser Arg Leu Leu Ala Ser Ala
 35 40 45
 Thr Pro Ile Gly Gly Ile Leu Leu Gly Leu Phe Asp Ala Ile Trp Gly
 50 55 60
 Ser Ile Gly Pro Ser Gln Trp Asp Leu Phe Leu Glu Gln Ile Glu Leu
 65 70 75 80
 Leu Ile Asp Gln Lys Ile Glu Glu Phe Ala Arg Asn Gln Ala Ile Ser

85

90

95

Arg Leu Glu Gly Ile Ser Ser Leu Tyr Gly Ile Tyr Thr Glu Ala Phe
100 105 110

Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Lys Glu Glu Met
115 120 125

Arg Thr Gln Phe Asn Asp Met Asn Ser Ile Leu Val Thr Ala Ile Pro
130 135 140

Leu Phe Ser Val Gln Asn Tyr Gln Val Pro Phe Leu Ser Val Tyr Val
145 150 155 160

Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser Val Phe
165 170 175

Gly Gln Ala Trp Gly Phe Asp Ile Ala Thr Ile Asn Ser Arg Tyr Asn
180 185 190

Asp Leu Thr Arg Leu Ile Pro Ile Tyr Thr Asp Tyr Ala Val Arg Trp
195 200 205

Tyr Asn Thr Gly Leu Asp Arg Leu Pro Arg Thr Gly Gly Leu Arg Asn
210 215 220

Trp Ala Arg Phe Asn Gln Phe Arg Arg Glu Leu Thr Ile Ser Val Leu
225 230 235 240

Asp Ile Ile Ser Phe Phe Arg Asn Tyr Asp Ser Arg Leu Tyr Pro Ile
245 250 255

Pro Thr Ser Ser Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Val Ile
260 265 270

Asn Ile Thr Asp Tyr Arg Val Gly Pro Ser Phe Glu Asn Ile Glu Asn
275 280 285

Ser Ala Ile Arg Ser Pro His Leu Met Asp Phe Leu Asn Asn Leu Thr
290 295 300

Ile Asp Thr Asp Leu Ile Arg Gly Val His Tyr Trp Ala Gly His Arg
305 310 315 320

Val Thr Ser His Phe Thr Gly Ser Ser Gln Val Ile Thr Thr Pro Gln
325 330 335

Tyr Gly Ile Thr Ala Asn Ala Glu Pro Arg Arg Thr Ile Ala Pro Ser
340 345 350

Thr Phe Pro Gly Leu Asn Leu Phe Tyr Arg Thr Leu Ser Asn Pro Phe
355 360 365

Phe Arg Arg Ser Glu Asn Ile Thr Pro Thr Leu Gly Ile Asn Val Val
 370 375 380
 Gln Gly Val Gly Phe Ile Gln Pro Asn Asn Ala Glu Val Leu Tyr Arg
 385 390 395 400
 Ser Arg Gly Thr Val Asp Ser Leu Asn Glu Leu Pro Ile Asp Gly Glu
 405 410 415
 Asn Ser Leu Val Gly Tyr Ser His Arg Leu Ser His Val Thr Leu Thr
 420 425 430
 Arg Ser Leu Tyr Asn Thr Asn Ile Thr Ser Leu Pro Thr Phe Val Trp
 435 440 445
 Thr His His Ser Ala Thr Asn Thr Asn Thr Ile Asn Pro Asp Ile Ile
 450 455 460
 Thr Gln Ile Pro Leu Val Lys Gly Phe Arg Leu Gly Gly Gly Thr Ser
 465 470 475 480
 Val Ile Lys Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Asn
 485 490 495
 Thr Ile Gly Glu Phe Val Ser Leu Gln Val Asn Ile Asn Ser Pro Ile
 500 505 510
 Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser Arg Asp Ala
 515 520 525
 Arg Ile Thr Val Ala Ile Gly Gly Gln Ile Arg Val Asp Met Thr Leu
 530 535 540
 Glu Lys Thr Met Glu Ile Gly Glu Ser Leu Thr Ser Arg Thr Phe Ser
 545 550 555 560
 Tyr Thr Asn Phe Ser Asn Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile
 565 570 575
 Ile Arg Ile Ala Glu Glu Leu Pro Ile Arg Gly Gly Glu Leu Tyr Ile
 580 585 590
 Asp Lys Ile Glu Leu Ile Leu Ala Asp Ala Thr Phe Glu Glu Glu Tyr
 595 600 605
 Asp Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Thr
 610 615 620
 Asn Gln Leu Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln
 625 630 635 640
 Val Ser Asn Leu Val Glu Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu
 645 650 655

Lys Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp
 660 665 670
 Glu Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln
 675 680 685
 Pro Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly
 690 695 700
 Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Phe Asp
 705 710 715 720
 Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu
 725 730 735
 Lys Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln
 740 745 750
 Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Val
 755 760 765
 Asn Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro
 770 775 780
 Ile Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp
 785 790 795 800
 Asn Pro Asn Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His
 805 810 815
 His Ser His His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu
 820 825 830
 Asn Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp
 835 840 845
 Gly Tyr Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Asn Pro Leu
 850 855 860
 Leu Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg
 865 870 875 880
 Asp Lys Cys Glu Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr Lys Glu
 885 890 895
 Ala Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg
 900 905 910
 Leu Gln Ala Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg
 915 920 925
 Val His Ser Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro

930 935 940
 Gly Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr
 945 950 955 960
 Ala Phe Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe
 965 970 975
 Asn Asn Gly Leu Ser Cys Trp Asn Val Lys Gly His Val Asp Val Glu
 980 985 990
 Glu Gln Asn Asn His Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala
 995 1000 1005
 Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu
 1010 1015 1020
 Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile
 1025 1030 1035 1040
 His Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val
 1045 1050 1055
 Glu Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr
 1060 1065 1070
 Ala Thr Gln Glu Glu His Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly
 1075 1080 1085
 Tyr Asp Glu Ala Tyr Glu Ser Asn Ser Ser Val His Ala Ser Val Tyr
 1090 1095 1100
 Glu Glu Lys Ser Tyr Thr Asp Arg Arg Arg Glu Asn Pro Cys Glu Ser
 1105 1110 1115 1120
 Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr
 1125 1130 1135
 Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile
 1140 1145 1150
 Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu Leu
 1155 1160 1165
 Met Glu Glu
 1170

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Hybrid sequence

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..3558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATG GAG ATA GTG AAT AAT CAG AAT CAA TGC GTG CCT TAT AAT TGT TTA	48
Met Glu Ile Val Asn Asn Gln Asn Gln Cys Val Pro Tyr Asn Cys Leu	
1 5 10 15	
AAT AAT CCT GAA AAT GAG ATA TTA GAT ATT GAA AGG TCA AAT AGT ACT	96
Asn Asn Pro Glu Asn Glu Ile Leu Asp Ile Glu Arg Ser Asn Ser Thr	
20 25 30	
GTA GCA ACA AAC ATC GCC TTG GAG ATT AGT CGT CTG CTC GCT TCC GCA	144
Val Ala Thr Asn Ile Ala Leu Glu Ile Ser Arg Leu Leu Ala Ser Ala	
35 40 45	
ACT CCA ATA GGG GGG ATT TTA TTA GGA TTG TTT GAT GCA ATA TGG GGG	192
Thr Pro Ile Gly Gly Ile Leu Leu Gly Leu Phe Asp Ala Ile Trp Gly	
50 55 60	
TCT ATA GGC CCT TCA CAA TGG GAT TTA TTT TTA GAG CAA ATT GAG CTA	240
Ser Ile Gly Pro Ser Gln Trp Asp Leu Phe Leu Glu Gln Ile Glu Leu	
65 70 75 80	
TTG ATT GAC CAA AAA ATA GAG GAA TTC GCT AGA AAC CAG GCA ATT TCT	288
Leu Ile Asp Gln Lys Ile Glu Glu Phe Ala Arg Asn Gln Ala Ile Ser	
85 90 95	
AGA TTG GAA GGG ATA AGC AGT CTG TAC GGA ATT TAT ACA GAA GCT TTT	336
Arg Leu Glu Gly Ile Ser Ser Leu Tyr Gly Ile Tyr Thr Glu Ala Phe	
100 105 110	
AGA GAG TGG GAA GCA GAT CCT ACT AAT CCA GCA TTA AAA GAA GAG ATG	384
Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Lys Glu Glu Met	
115 120 125	
CGT ACT CAA TTT AAT GAC ATG AAC AGT ATT CTT GTA ACA GCT ATT CCT	432
Arg Thr Gln Phe Asn Asp Met Asn Ser Ile Leu Val Thr Ala Ile Pro	
130 135 140	

CTT TTT TCA GTT CAA AAT TAT CAA GTC CCA TTT TTA TCA GTA TAT GTT 480
 Leu Phe Ser Val Gln Asn Tyr Gln Val Pro Phe Leu Ser Val Tyr Val
 145 150 155 160

CAA GCT GCA AAT TTA CAT TTA TCG GTT TTG AGA GAT GTT TCA GTG TTT 528
 Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser Val Phe
 165 170 175

GGG CAG GCT TGG GGA TTT GAT ATA GCA ACA ATA AAT AGT CGT TAT AAT 576
 Gly Gln Ala Trp Gly Phe Asp Ile Ala Thr Ile Asn Ser Arg Tyr Asn
 180 185 190

GAT CTG ACT AGA CTT ATT CCT ATA TAT ACA GAT TAT GCT GTA CGC TGG 624
 Asp Leu Thr Arg Leu Ile Pro Ile Tyr Thr Asp Tyr Ala Val Arg Trp
 195 200 205

TAC AAT ACG GGA TTA GAT CGC TTA CCA CGA ACT GGT GGG CTG CGA AAC 672
 Tyr Asn Thr Gly Leu Asp Arg Leu Pro Arg Thr Gly Gly Leu Arg Asn
 210 215 220

TGG GCA AGA TTT AAT CAG TTT AGA AGA GAG TTA ACA ATA TCA GTA TTA 720
 Trp Ala Arg Phe Asn Gln Phe Arg Arg Glu Leu Thr Ile Ser Val Leu
 225 230 235 240

GAT ATT ATT TCT TTT TTC AGA AAT TAC GAT TCT AGA TTA TAT CCA ATT 768
 Asp Ile Ile Ser Phe Phe Arg Asn Tyr Asp Ser Arg Leu Tyr Pro Ile
 245 250 255

CCA ACA AGC TCC CAA TTA ACG CGG GAA GTA TAT ACA GAT CCG GTA ATT 816
 Pro Thr Ser Ser Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Val Ile
 260 265 270

AAT ATA ACT GAC TAT AGA GTT GGC CCC AGC TTC GAG AAT ATT GAG AAC 864
 Asn Ile Thr Asp Tyr Arg Val Gly Pro Ser Phe Glu Asn Ile Glu Asn
 275 280 285

TCA GCC ATT AGA AGC CCC CAC CTT ATG GAC TTC TTA AAT AAT TTG ACC 912
 Ser Ala Ile Arg Ser Pro His Leu Met Asp Phe Leu Asn Asn Leu Thr
 290 295 300

ATT GAT ACG GAT TTG ATT AGA GGT GTT CAC TAT TGG GCA GGG CAT CGT 960
 Ile Asp Thr Asp Leu Ile Arg Gly Val His Tyr Trp Ala Gly His Arg
 305 310 315 320

GTA ACT TCT CAT TTT ACA GGT AGT TCT CAA GTG ATA ACA ACC CCT CAA 1008
 Val Thr Ser His Phe Thr Gly Ser Ser Gln Val Ile Thr Thr Pro Gln
 325 330 335

TAT GGG ATA ACC GCA AAT GCG GAA CCA AGA CGA ACT ATT GCT CCT AGT 1056
 Tyr Gly Ile Thr Ala Asn Ala Glu Pro Arg Arg Thr Ile Ala Pro Ser
 340 345 350

002260-053320

ACT TTT CCA GGT CTT AAC CTA TTT TAT AGA ACA TTA TCA AAT CCT TTC 1104
 Thr Phe Pro Gly Leu Asn Leu Phe Tyr Arg Thr Leu Ser Asn Pro Phe
 355 360 365

TTC CGA AGA TCA GAA AAT ATT ACT CCT ACC TTA GGG ATA AAT GTA GTA 1152
 Phe Arg Arg Ser Glu Asn Ile Thr Pro Thr Leu Gly Ile Asn Val Val
 370 375 380

CAG GGA GTA GGG TTC ATT CAA CCA AAT AAT GCT GAA GTT CTA TAT AGA 1200
 Gln Gly Val Gly Phe Ile Gln Pro Asn Asn Ala Glu Val Leu Tyr Arg
 385 390 395 400

AGT AGG GGG ACA GTA GAT TCT CTT AAT GAG TTA CCA ATT GAT GGT GAG 1248
 Ser Arg Gly Thr Val Asp Ser Leu Asn Glu Leu Pro Ile Asp Gly Glu
 405 410 415

AAT TCA TTA GTT GGA TAT AGT CAT CGA TTA AGT CAT GTT ACA CTA ACC 1296
 Asn Ser Leu Val Gly Tyr Ser His Arg Leu Ser His Val Thr Leu Thr
 420 425 430

AGG TCG TTA TAT AAT ACT AAT ATA ACT AGC CTG CCA ACA TTT GTT TGG 1344
 Arg Ser Leu Tyr Asn Thr Asn Ile Thr Ser Leu Pro Thr Phe Val Trp
 435 440 445

ACA CAT CAC AGT GCT ACT AAT ACA AAT ACA ATT AAT CCA GAT ATT ATT 1392
 Thr His His Ser Ala Thr Asn Thr Asn Thr Ile Asn Pro Asp Ile Ile
 450 455 460

ACA CAA ATA CCT TTA GTG AAA GGA TTT AGA GTT TGG GGG GGC ACC TCT 1440
 Thr Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly Gly Thr Ser
 465 470 475 480

GTC ATT ACA GGA CCA GGA TTT ACA GGA GGG GAT ATC CTT CGA AGA AAT 1488
 Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Asn
 485 490 495

ACC TTT GGT GAT TTT GTA TCT CTA CAA GTC AAT ATT AAT TCA CCA ATT 1536
 Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn Ser Pro Ile
 500 505 510

ACC CAA AGA TAC CGT TTA AGA TTT CGT TAC GCT TCC AGT AGG GAT GCA 1584
 Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser Arg Asp Ala
 515 520 525

CGA GTT ATA GTA TTA ACA GGA GCG GCA TCC ACA GGA GTG GGA GGC CAA 1632
 Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val Gly Gly Gln
 530 535 540

GTT AGT GTA AAT ATG CCT CTT CAG AAA ACT ATG GAA ATA GGG GAG AAC 1680
 Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile Gly Glu Asn
 545 550 555 560

TTA ACA TCT AGA ACA TTT AGA TAT ACC GAT TTT AGT AAT CCT TTT TCA 1728

Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn Pro Phe Ser
 565 570 575

TTT AGA GCT AAT CCA GAT ATA ATT GGG ATA AGT GAA CAA CCT CTA TTT 1776
 Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln Pro Leu Phe
 580 585 590

GGT GCA GGT TCT ATT AGT AGC GGT GAA CTT TAT ATA GAT AAA ATT GAA 1824
 Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp Lys Ile Glu
 595 600 605

ATT ATT CTA GCA GAT GCA ACA TTT GAA GCA GAA TCT GAT TTA GAA AGA 1872
 Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp Leu Glu Arg
 610 615 620

GCA CAA AAG GCG GTG AAT GCC CTG TTT ACT TCT TCC AAT CAA ATC GGG 1920
 Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn Gln Ile Gly
 625 630 635 640

TTA AAA ACC GAT GTG ACG GAT TAT CAT ATT GAT CAA GTA TCC AAT TTA 1968
 Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu
 645 650 655

GTG GAT TGT TTA TCA GAT GAA TTT TGT CTG GAT GAA AAG CGA GAA TTG 2016
 Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu
 660 665 670

TCC GAG AAA GTC AAA CAT GCG AAG CGA CTC AGT GAT GAG CGG AAT TTA 2064
 Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu
 675 680 685

CTT CAA GAT CCA AAC TTC AGA GGG ATC AAT AGA CAA CCA GAC CGT GGC 2112
 Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro Asp Arg Gly
 690 695 700

TGG AGA GGA AGT ACA GAT ATT ACC ATC CAA GGA GGA GAT GAC GTA TTC 2160
 Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe
 705 710 715 720

AAA GAG AAT TAC GTC ACA CTA CCG GGT ACC GTT GAT GAG TGC TAT CCA 2208
 Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu Cys Tyr Pro
 725 730 735

ACG TAT TTA TAT CAG AAA ATA GAT GAG TCG AAA TTA AAA GCT TAT ACC 2256
 Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr
 740 745 750

CGT TAT GAA TTA AGA GGG TAT ATC GAA GAT AGT CAA GAC TTA GAA ATC 2304
 Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile
 755 760 765

TAT TTG ATC CGT TAC AAT GCA AAA CAC GAA ATA GTA AAT GTG CCA GGC 2352
 Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn Val Pro Gly

770	775	780	
ACG GGT TCC TTA TGG CCG CTT TCA GCC CAA AGT CCA ATC GGA AAG TGT			2400
Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys			
785	790	795	800
GGA GAA CCG AAT CGA TGC GCG CCA CAC CTT GAA TGG AAT CCT GAT CTA			2448
Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu			
	805	810	815
GAT TGT TCC TGC AGA GAC GGG GAA AAA TGT GCA CAT CAT TCC CAT CAT			2496
Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His Ser His His			
	820	825	830
TTC ACC TTG GAT ATT GAT GTT GGA TGT ACA GAC TTA AAT GAG GAC TTA			2544
Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu			
	835	840	845
GGT GTA TGG GTG ATA TTC AAG ATT AAG ACG CAA GAT GGC CAT GCA AGA			2592
Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg			
	850	855	860
CTA GGG AAT CTA GAG TTT CTC GAA GAG AAA CCA TTA TTA GGG GAA GCA			2640
Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu Gly Glu Ala			
	865	870	875
CTA GCT CGT GTG AAA AGA GCG GAG AAG AAG TGG AGA GAC AAA CGA GAG			2688
Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu			
	885	890	895
AAA CTG CAG TTG GAA ACA AAT ATT GTT TAT AAA GAG GCA AAA GAA TCT			2736
Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser			
	900	905	910
GTA GAT GCT TTA TTT GTA AAC TCT CAA TAT GAT AGA TTA CAA GTG GAT			2784
Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu Gln Val Asp			
	915	920	925
ACG AAC ATC GCG ATG ATT CAT GCG GCA GAT AAA CGC GTT CAT AGA ATC			2832
Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val His Arg Ile			
	930	935	940
CGG GAA GCG TAT CTG CCA GAG TTG TCT GTG ATT CCA GGT GTC AAT GCG			2880
Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala			
	945	950	955
GCC ATT TTC GAA GAA TTA GAG GGA CGT ATT TTT ACA GCG TAT TCC TTA			2928
Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala Tyr Ser Leu			
	965	970	975
TAT GAT GCG AGA AAT GTC ATT AAA AAT GGC GAT TTC AAT AAT GGC TTA			2976
Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu			
	980	985	990

TTA TGC TGG AAC GTG AAA GGT CAT GTA GAT GTA GAA GAG CAA AAC AAC 3024
 Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu Gln Asn Asn
 995 1000 1005

CAC CGT TCG GTC CTT GTT ATC CCA GAA TGG GAG GCA GAA GTG TCA CAA 3072
 His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu Val Ser Gln
 1010 1015 1020

GAG GTT CGT GTC TGT CCA GGT CGT GGC TAT ATC CTT CGT GTC ACA GCA 3120
 Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala
 1025 1030 1035 1040

TAT AAA GAG GGA TAT GGA GAG GGC TGC GTA ACG ATC CAT GAG ATC GAA 3168
 Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu
 1045 1050 1055

GAC AAT ACA GAC GAA CTG AAA TTC AGC AAC TGT GTA GAA GAG GAA GTA 3216
 Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val
 1060 1065 1070

TAT CCA AAC AAC ACA GTA ACG TGT AAT AAT TAT ACT GGG ACT CAA GAA 3264
 Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly Thr Gln Glu
 1075 1080 1085

GAA TAT GAG GGT ACG TAC ACT TCT CGT AAT CAA GGA TAT GAC GAA GCC 3312
 Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr Asp Glu Ala
 1090 1095 1100

TAT GGT AAT AAC CCT TCC GTA CCA GCT GAT TAC GCT TCA GTC TAT GAA 3360
 Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser Val Tyr Glu
 1105 1110 1115 1120

GAA AAA TCG TAT ACA GAT GGA CGA AGA GAG AAT CCT TGT GAA TCT AAC 3408
 Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys Glu Ser Asn
 1125 1130 1135

AGA GGC TAT GGG GAT TAC ACA CCA CTA CCG GCT GGT TAT GTA ACA AAG 3456
 Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys
 1140 1145 1150

GAT TTA GAG TAC TTC CCA GAG ACC GAT AAG GTA TGG ATT GAG ATC GGA 3504
 Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly
 1155 1160 1165

GAA ACA GAA GGA ACA TTC ATC GTG GAT AGC GTG GAA TTA CTC CTT ATG 3552
 Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met
 1170 1175 1180

GAG GAA 3558
 Glu Glu
 1185

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1186 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Glu Ile Val Asn Asn Gln Asn Gln Cys Val Pro Tyr Asn Cys Leu
 1 5 10 15

Asn Asn Pro Glu Asn Glu Ile Leu Asp Ile Glu Arg Ser Asn Ser Thr
 20 25 30

Val Ala Thr Asn Ile Ala Leu Glu Ile Ser Arg Leu Leu Ala Ser Ala
 35 40 45

Thr Pro Ile Gly Gly Ile Leu Leu Gly Leu Phe Asp Ala Ile Trp Gly
 50 55 60

Ser Ile Gly Pro Ser Gln Trp Asp Leu Phe Leu Glu Gln Ile Glu Leu
 65 70 75 80

Leu Ile Asp Gln Lys Ile Glu Glu Phe Ala Arg Asn Gln Ala Ile Ser
 85 90 95

Arg Leu Glu Gly Ile Ser Ser Leu Tyr Gly Ile Tyr Thr Glu Ala Phe
 100 105 110

Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Lys Glu Glu Met
 115 120 125

Arg Thr Gln Phe Asn Asp Met Asn Ser Ile Leu Val Thr Ala Ile Pro
 130 135 140

Leu Phe Ser Val Gln Asn Tyr Gln Val Pro Phe Leu Ser Val Tyr Val
 145 150 155 160

Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser Val Phe
 165 170 175

Gly Gln Ala Trp Gly Phe Asp Ile Ala Thr Ile Asn Ser Arg Tyr Asn
 180 185 190

Asp Leu Thr Arg Leu Ile Pro Ile Tyr Thr Asp Tyr Ala Val Arg Trp
 195 200 205

Tyr Asn Thr Gly Leu Asp Arg Leu Pro Arg Thr Gly Gly Leu Arg Asn
 210 215 220

Trp Ala Arg Phe Asn Gln Phe Arg Arg Glu Leu Thr Ile Ser Val Leu
 225 230 235 240
 Asp Ile Ile Ser Phe Phe Arg Asn Tyr Asp Ser Arg Leu Tyr Pro Ile
 245 250 255
 Pro Thr Ser Ser Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Val Ile
 260 265 270
 Asn Ile Thr Asp Tyr Arg Val Gly Pro Ser Phe Glu Asn Ile Glu Asn
 275 280 285
 Ser Ala Ile Arg Ser Pro His Leu Met Asp Phe Leu Asn Asn Leu Thr
 290 295 300
 Ile Asp Thr Asp Leu Ile Arg Gly Val His Tyr Trp Ala Gly His Arg
 305 310 315 320
 Val Thr Ser His Phe Thr Gly Ser Ser Gln Val Ile Thr Thr Pro Gln
 325 330 335
 Tyr Gly Ile Thr Ala Asn Ala Glu Pro Arg Arg Thr Ile Ala Pro Ser
 340 345 350
 Thr Phe Pro Gly Leu Asn Leu Phe Tyr Arg Thr Leu Ser Asn Pro Phe
 355 360 365
 Phe Arg Arg Ser Glu Asn Ile Thr Pro Thr Leu Gly Ile Asn Val Val
 370 375 380
 Gln Gly Val Gly Phe Ile Gln Pro Asn Asn Ala Glu Val Leu Tyr Arg
 385 390 395 400
 Ser Arg Gly Thr Val Asp Ser Leu Asn Glu Leu Pro Ile Asp Gly Glu
 405 410 415
 Asn Ser Leu Val Gly Tyr Ser His Arg Leu Ser His Val Thr Leu Thr
 420 425 430
 Arg Ser Leu Tyr Asn Thr Asn Ile Thr Ser Leu Pro Thr Phe Val Trp
 435 440 445
 Thr His His Ser Ala Thr Asn Thr Asn Thr Ile Asn Pro Asp Ile Ile
 450 455 460
 Thr Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly Gly Thr Ser
 465 470 475 480
 Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Asn
 485 490 495
 Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn Ser Pro Ile

500

505

510

Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser Arg Asp Ala
515 520 525

Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val Gly Gly Gln
530 535 540

Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile Gly Glu Asn
545 550 555 560

Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn Pro Phe Ser
565 570 575

Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln Pro Leu Phe
580 585 590

Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp Lys Ile Glu
595 600 605

Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp Leu Glu Arg
610 615 620

Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn Gln Ile Gly
625 630 635 640

Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu
645 650 655

Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu
660 665 670

Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu
675 680 685

Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro Asp Arg Gly
690 695 700

Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe
705 710 715 720

Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu Cys Tyr Pro
725 730 735

Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr
740 745 750

Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile
755 760 765

Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn Val Pro Gly
770 775 780

Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys
 785 790 795 800
 Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu
 805 810 815
 Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His Ser His His
 820 825 830
 Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu
 835 840 845
 Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg
 850 855 860
 Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu Gly Glu Ala
 865 870 875 880
 Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu
 885 890 895
 Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser
 900 905 910
 Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu Gln Val Asp
 915 920 925
 Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val His Arg Ile
 930 935 940
 Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala
 945 950 955 960
 Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala Tyr Ser Leu
 965 970 975
 Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu
 980 985 990
 Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu Gln Asn Asn
 995 1000 1005
 His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu Val Ser Gln
 1010 1015 1020
 Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala
 1025 1030 1035 1040
 Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu
 1045 1050 1055
 Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val
 1060 1065 1070

Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly Thr Gln Glu
 1075 1080 1085
 Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr Asp Glu Ala
 1090 1095 1100
 Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser Val Tyr Glu
 1105 1110 1115 1120
 Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys Glu Ser Asn
 1125 1130 1135
 Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys
 1140 1145 1150
 Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly
 1155 1160 1165
 Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met
 1170 1175 1180
 Glu Glu
 1185

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Hybrid toxin

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATG GAT AAC AAT CCG AAC ATC AAT GAA TGC ATT CCT TAT AAT TGT TTA
 Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
 1 5 10 15

48

AGT AAC CCT GAA GTA GAA GTA TTA GGT GGA GAA AGA ATA GAA ACT GGT Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly 20 25 30	96
TAC ACC CCA ATC GAT ATT TCC TTG TCG CTA ACG CAA TTT CTT TTG AGT Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser 35 40 45	144
GAA TTT GTT CCC GGT GCT GGA TTT GTG TTA GGA CTA GTT GAT ATA ATA Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile 50 55 60	192
TGG GGA ATT TTT GGT CCC TCT CAA TGG GAC GCA TTT CTT GTA CAA ATT Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile 65 70 75 80	240
GAA CAG TTA ATT AAC CAA AGA ATA GAA GAA TTC GCT AGG AAC CAA GCC Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 85 90 95	288
ATT TCT AGA TTA GAA GGA CTA AGC AAT CTT TAT CAA ATT TAC GCA GAA Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 100 105 110	336
TCT TTT AGA GAG TGG GAA GCA GAT CCT ACT AAT CCA GCA TTA AGA GAA Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 115 120 125	384
GAG ATG CGT ATT CAA TTC AAT GAC ATG AAC AGT GCC CTT ACA ACC GCT Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 130 135 140	432
ATT CCT CTT TTT GCA GTT CAA AAT TAT CAA GTT CCT CTT TTA TCA GTA Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 145 150 155 160	480
TAT GTT CAA GCT GCA AAT TTA CAT TTA TCA GTT TTG AGA GAT GTT TCA Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 165 170 175	528
GTG TTT GGA CAA AGG TGG GGA TTT GAT GCC GCG ACT ATC AAT AGT CGT Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 180 185 190	576
TAT AAT GAT TTA ACT AGG CTT ATT GGC AAC TAT ACA GAT CAT GCT GTA Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val 195 200 205	624
CGC TGG TAC AAT ACG GGA TTA GAG CGT GTA TGG GGA CCG GAT TCT AGA Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 210 215 220	672
GAT TGG ATA AGA TAT AAT CAA TTT AGA AGA GAA TTA ACA CTA ACT GTA	720

Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val	
225 230 235 240	
TTA GAT ATC GTT TCT CTA TTT CCG AAC TAT GAT AGT AGA ACG TAT CCA	768
Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro	
245 250 255	
ATT CGA ACA GTT TCC CAA TTA ACA AGA GAA ATT TAT ACA AAC CCA GTA	816
Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val	
260 265 270	
TTA GAA AAT TTT GAT GGT AGT TTT CGA GGC TCG GCT CAG GGC ATA GAA	864
Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu	
275 280 285	
GGA AGT ATT AGG AGT CCA CAT TTG ATG GAT ATA CTT AAC AGT ATA ACC	912
Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr	
290 295 300	
ATC TAT ACG GAT GCT CAT AGA GGA GAA TAT TAT TGG TCA GGG CAT CAA	960
Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln	
305 310 315 320	
ATA ATG GCT TCT CCT GTA GGG TTT TCG GGG CCA GAA TTC ACT TTT CCG	1008
Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro	
325 330 335	
CTA TAT GGA ACT ATG GGA AAT GCA GCT CCA CAA CAA CGT ATT GTT GCT	1056
Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala	
340 345 350	
CAA CTA GGT CAG GGC GTG TAT AGA ACA TTA TCG TCC ACT TTA TAT AGA	1104
Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg	
355 360 365	
AGA CCT TTT AAT ATA GGG ATA AAT AAT CAA CAA CTA TCT GTT CTT GAC	1152
Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp	
370 375 380	
GGG ACA GAA TTT GCT TAT GGA ACC TCC TCA AAT TTG CCA TCC GCT GTA	1200
Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val	
385 390 395 400	
TAC AGA AAA AGC GGA ACG GTA GAT TCG CTG GAT GAA ATA CCG CCA CAG	1248
Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln	
405 410 415	
AAT AAC AAC GTG CCA CCT AGG CAA GGA TTT AGT CAT CGA TTA AGC CAT	1296
Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His	
420 425 430	
GTT TCA ATG TTT CGT TCA GGC TTT AGT AAT AGT AGT GTA AGT ATA ATA	1344
Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile	

56

ATT GAT CAA GTA TCC AAT TTA GTG GAT TGT TTA TCA GAT GAA TTT TGT 2016
 Ile Asp Gln Val Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys
 660 665 670

CTG GAT GAA AAG CGA GAA TTG TCC GAG AAA GTC AAA CAT GCG AAG CGA 2064
 Leu Asp Glu Lys Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg
 675 680 685

CTC AGT GAT GAG CGG AAT TTA CTT CAA GAT CCA AAC TTC AGA GGG ATC 2112
 Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile
 690 695 700

AAT AGA CAA CCA GAC CGT GGC TGG AGA GGA AGT ACA GAT ATT ACC ATC 2160
 Asn Arg Gln Pro Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile
 705 710 715 720

CAA GGA GGA GAT GAC GTA TTC AAA GAG AAT TAC GTC ACA CTA CCG GGT 2208
 Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly
 725 730 735

ACC GTT GAT GAG TGC TAT CCA ACG TAT TTA TAT CAG AAA ATA GAT GAG 2256
 Thr Val Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu
 740 745 750

TCG AAA TTA AAA GCT TAT ACC CGT TAT GAA TTA AGA GGG TAT ATC GAA 2304
 Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu
 755 760 765

GAT AGT CAA GAC TTA GAA ATC TAT TTG ATC CGT TAC AAT GCA AAA CAC 2352
 Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His
 770 775 780

GAA ATA GTA AAT GTG CCA GGC ACG GGT TCC TTA TGG CCG CTT TCA GCC 2400
 Glu Ile Val Asn Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala
 785 790 795 800

CAA AGT CCA ATC GGA AAG TGT GGA GAA CCG AAT CGA TGC GCG CCA CAC 2448
 Gln Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His
 805 810 815

CTT GAA TGG AAT CCT GAT CTA GAT TGT TCC TGC AGA GAC GGG GAA AAA 2496
 Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys
 820 825 830

TGT GCA CAT CAT TCC CAT CAT TTC ACC TTG GAT ATT GAT GTT GGA TGT 2544
 Cys Ala His His Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys
 835 840 845

ACA GAC TTA AAT GAG GAC TTA GGT GTA TGG GTG ATA TTC AAG ATT AAG 2592
 Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys
 850 855 860

ACG CAA GAT GGC CAT GCA AGA CTA GGG AAT CTA GAG TTT CTC GAA GAG 2640
 Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu
 865 870 875 880

AAA CCA TTA TTA GGG GAA GCA CTA GCT CGT GTG AAA AGA GCG GAG AAG 2688
 Lys Pro Leu Leu Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys
 885 890 895

AAG TGG AGA GAC AAA CGA GAG AAA CTG CAG TTG GAA ACA AAT ATT GTT 2736
 Lys Trp Arg Asp Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val
 900 905 910

TAT AAA GAG GCA AAA GAA TCT GTA GAT GCT TTA TTT GTA AAC TCT CAA 2784
 Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln
 915 920 925

TAT GAT AGA TTA CAA GTG GAT ACG AAC ATC GCG ATG ATT CAT GCG GCA 2832
 Tyr Asp Arg Leu Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala
 930 935 940

GAT AAA CGC GTT CAT AGA ATC CGG GAA GCG TAT CTG CCA GAG TTG TCT 2880
 Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser
 945 950 955 960

GTG ATT CCA GGT GTC AAT GCG GCC ATT TTC GAA GAA TTA GAG GGA CGT 2928
 Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg
 965 970 975

ATT TTT ACA GCG TAT TCC TTA TAT GAT GCG AGA AAT GTC ATT AAA AAT 2976
 Ile Phe Thr Ala Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn
 980 985 990

GGC GAT TTC AAT AAT GGC TTA TTA TGC TGG AAC GTG AAA GGT CAT GTA 3024
 Gly Asp Phe Asn Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val
 995 1000 1005

GAT GTA GAA GAG CAA AAC AAC CAC CGT TCG GTC CTT GTT ATC CCA GAA 3072
 Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu
 1010 1015 1020

TGG GAG GCA GAA GTG TCA CAA GAG GTT CGT GTC TGT CCA GGT CGT GGC 3120
 Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly
 1025 1030 1035 1040

TAT ATC CTT CGT GTC ACA GCA TAT AAA GAG GGA TAT GGA GAG GGC TGC 3168
 Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys
 1045 1050 1055

GTA ACG ATC CAT GAG ATC GAA GAC AAT ACA GAC GAA CTG AAA TTC AGC 3216
 Val Thr Ile His Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser
 1060 1065 1070

AAC TGT GTA GAA GAG GAA GTA TAT CCA AAC AAC ACA GTA ACG TGT AAT 3264

Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn
 1075 1080 1085

AAT TAT ACT GGG ACT CAA GAA GAA TAT GAG GGT ACG TAC ACT TCT CGT 3312
 Asn Tyr Thr Gly Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg
 1090 1095 1100

AAT CAA GGA TAT GAC GAA GCC TAT GGT AAT AAC CCT TCC GTA CCA GCT 3360
 Asn Gln Gly Tyr Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala
 1105 1110 1115 1120

GAT TAC GCT TCA GTC TAT GAA GAA AAA TCG TAT ACA GAT GGA CGA AGA 3408
 Asp Tyr Ala Ser Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg
 1125 1130 1135

GAG AAT CCT TGT GAA TCT AAC AGA GGC TAT GGG GAT TAC ACA CCA CTA 3456
 Glu Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu
 1140 1145 1150

CCG GCT GGT TAT GTA ACA AAG GAT TTA GAG TAC TTC CCA GAG ACC GAT 3504
 Pro Ala Gly Tyr Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp
 1155 1160 1165

AAG GTA TGG ATT GAG ATC GGA GAA ACA GAA GGA ACA TTC ATC GTG GAT 3552
 Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp
 1170 1175 1180

AGC GTG GAA TTA CTC CTT ATG GAG GAA 3579
 Ser Val Glu Leu Leu Leu Met Glu Glu
 1185 1190

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
 1 5 10 15

Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
 20 25 30

Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
 35 40 45

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile

50 55 60
 Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
 65 70 75 80
 Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
 85 90 95
 Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
 100 105 110
 Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
 115 120 125
 Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
 130 135 140
 Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
 145 150 155 160
 Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
 165 170 175
 Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
 180 185 190
 Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val
 195 200 205
 Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
 210 215 220
 Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
 225 230 235 240
 Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro
 245 250 255
 Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
 260 265 270
 Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
 275 280 285
 Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
 290 295 300
 Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln
 305 310 315 320
 Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
 325 330 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
 340 345 350
 Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
 355 360 365
 Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
 370 375 380
 Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
 385 390 395 400
 Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
 405 410 415
 Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
 420 425 430
 Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
 435 440 445
 Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Thr Leu Thr Asn
 450 455 460
 Thr Ile Asp Pro Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe
 465 470 475 480
 Arg Val Trp Gly Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly
 485 490 495
 Gly Asp Ile Leu Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln
 500 505 510
 Val Asn Ile Asn Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg
 515 520 525
 Tyr Ala Ser Ser Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala
 530 535 540
 Ser Thr Gly Val Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys
 545 550 555 560
 Thr Met Glu Ile Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr
 565 570 575
 Asp Phe Ser Asn Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly
 580 585 590
 Ile Ser Glu Gln Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu
 595 600 605
 Leu Tyr Ile Asp Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu
 610 615 620

Ala Glu Ser Asp Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe
 625 630 635 640
 Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His
 645 650 655
 Ile Asp Gln Val Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys
 660 665 670
 Leu Asp Glu Lys Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg
 675 680 685
 Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile
 690 695 700
 Asn Arg Gln Pro Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile
 705 710 715 720
 Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly
 725 730 735
 Thr Val Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu
 740 745 750
 Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu
 755 760 765
 Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His
 770 775 780
 Glu Ile Val Asn Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala
 785 790 795 800
 Gln Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His
 805 810 815
 Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys
 820 825 830
 Cys Ala His His Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys
 835 840 845
 Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys
 850 855 860
 Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu
 865 870 875 880
 Lys Pro Leu Leu Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys
 885 890 895
 Lys Trp Arg Asp Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val

900	905	910
Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln 915	920	925
Tyr Asp Arg Leu Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala 930	935	940
Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser 945	950	955 960
Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg 965	970	975
Ile Phe Thr Ala Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn 980	985	990
Gly Asp Phe Asn Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val 995	1000	1005
Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu 1010	1015	1020
Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly 1025	1030	1035 1040
Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys 1045	1050	1055
Val Thr Ile His Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser 1060	1065	1070
Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn 1075	1080	1085
Asn Tyr Thr Gly Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg 1090	1095	1100
Asn Gln Gly Tyr Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala 1105	1110	1115 1120
Asp Tyr Ala Ser Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg 1125	1130	1135
Glu Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu 1140	1145	1150
Pro Ala Gly Tyr Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp 1155	1160	1165
Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp 1170	1175	1180

Ser Val Glu Leu Leu Leu Met Glu Glu
1185 1190

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG AAT CAA AAT AAA CAC GGA ATT ATT GGC GCT TCC AAT TGT GGT TGT	48
Met Asn Gln Asn Lys His Gly Ile Ile Gly Ala Ser Asn Cys Gly Cys	
1 5 10 15	
GCA TCT GAT GAT GTT GCG AAA TAT CCT TTA GCC AAC AAT CCA TAT TCA	96
Ala Ser Asp Asp Val Ala Lys Tyr Pro Leu Ala Asn Asn Pro Tyr Ser	
20 25 30	
TCT GCT TTA AAT TTA AAT TCT TGT CAA AAT AGT AGT ATT CTC AAC TGG	144
Ser Ala Leu Asn Leu Asn Ser Cys Gln Asn Ser Ser Ile Leu Asn Trp	
35 40 45	
ATT AAC ATA ATA GGC GAT GCA GCA AAA GAA GCA GTA TCT ATT GGG ACA	192
Ile Asn Ile Ile Gly Asp Ala Ala Lys Glu Ala Val Ser Ile Gly Thr	
50 55 60	
ACC ATA GTC TCT CTT ATC ACA GCA CCT TCT CTT ACT GGA TTA ATT TCA	240
Thr Ile Val Ser Leu Ile Thr Ala Pro Ser Leu Thr Gly Leu Ile Ser	
65 70 75 80	
ATA GTA TAT GAC CTT ATA GGT AAA GTA CTA GGA GGT AGT AGT GGA CAA	288
Ile Val Tyr Asp Leu Ile Gly Lys Val Leu Gly Gly Ser Ser Gly Gln	
85 90 95	
TCC ATA TCA GAT TTG TCT ATA TGT GAC TTA TTA TCT ATT ATT GAT TTA	336
Ser Ile Ser Asp Leu Ser Ile Cys Asp Leu Leu Ser Ile Ile Asp Leu	
100 105 110	
CGG GTA AGT CAG AGT GTT TTA AAT GAT GGG ATT GCA GAT TTT AAT GGT	384

Arg	Val	Ser	Gln	Ser	Val	Leu	Asn	Asp	Gly	Ile	Ala	Asp	Phe	Asn	Gly	
	115						120					125				
TCT	GTA	CTC	TTA	TAC	AGG	AAC	TAT	TTA	GAG	GCT	CTG	GAT	AGC	TGG	AAT	432
Ser	Val	Leu	Leu	Tyr	Arg	Asn	Tyr	Leu	Glu	Ala	Leu	Asp	Ser	Trp	Asn	
	130					135					140					
AAG	AAT	CCT	AAT	TCT	GCT	TCT	GCT	GAA	GAA	CTC	CGT	ACT	CGT	TTT	AGA	480
Lys	Asn	Pro	Asn	Ser	Ala	Ser	Ala	Glu	Glu	Leu	Arg	Thr	Arg	Phe	Arg	
145					150					155					160	
ATC	GCC	GAC	TCA	GAA	TTT	GAT	AGA	ATT	TTA	ACC	CGA	GGG	TCT	TTA	ACG	528
Ile	Ala	Asp	Ser	Glu	Phe	Asp	Arg	Ile	Leu	Thr	Arg	Gly	Ser	Leu	Thr	
				165					170					175		
AAT	GGT	GGC	TCG	TTA	GCT	AGA	CAA	AAT	GCC	CAA	ATA	TTA	TTA	TTA	CCT	576
Asn	Gly	Gly	Ser	Leu	Ala	Arg	Gln	Asn	Ala	Gln	Ile	Leu	Leu	Leu	Pro	
			180					185					190			
TCT	TTT	GCG	AGC	GCT	GCA	TTT	TTC	CAT	TTA	TTA	CTA	CTA	AGG	GAT	GCT	624
Ser	Phe	Ala	Ser	Ala	Ala	Phe	Phe	His	Leu	Leu	Leu	Leu	Arg	Asp	Ala	
	195						200					205				
ACT	AGA	TAT	GGC	ACT	AAT	TGG	GGG	CTA	TAC	AAT	GCT	ACA	CCT	TTT	ATA	672
Thr	Arg	Tyr	Gly	Thr	Asn	Trp	Gly	Leu	Tyr	Asn	Ala	Thr	Pro	Phe	Ile	
	210					215				220						
AAT	TAT	CAA	TCA	AAA	CTA	GTA	GAG	CTT	ATT	GAA	CTA	TAT	ACT	GAT	TAT	720
Asn	Tyr	Gln	Ser	Lys	Leu	Val	Glu	Leu	Ile	Glu	Leu	Tyr	Thr	Asp	Tyr	
225					230					235					240	
TGC	GTA	CAT	TGG	TAT	AAT	CGA	GGT	TTC	AAC	GAA	CTA	AGA	CAA	CGA	GGC	768
Cys	Val	His	Trp	Tyr	Asn	Arg	Gly	Phe	Asn	Glu	Leu	Arg	Gln	Arg	Gly	
			245					250					255			
ACT	AGT	GCT	ACA	GCT	TGG	TTA	GAA	TTT	CAT	AGA	TAT	CGT	AGA	GAG	ATG	816
Thr	Ser	Ala	Thr	Ala	Trp	Leu	Glu	Phe	His	Arg	Tyr	Arg	Arg	Glu	Met	
			260				265					270				
ACA	TTG	ATG	GTA	TTA	GAT	ATA	GTA	GCA	TCA	TTT	TCA	AGT	CTT	GAT	ATT	864
Thr	Leu	Met	Val	Leu	Asp	Ile	Val	Ala	Ser	Phe	Ser	Ser	Leu	Asp	Ile	
	275					280						285				
ACT	AAT	TAC	CCA	ATA	GAA	ACA	GAT	TTT	CAG	TTG	AGT	AGG	GTC	ATT	TAT	912
Thr	Asn	Tyr	Pro	Ile	Glu	Thr	Asp	Phe	Gln	Leu	Ser	Arg	Val	Ile	Tyr	
	290					295					300					
ACA	GAT	CCA	ATT	GGT	TTT	GTA	CAT	CGT	AGT	AGT	CTT	AGG	GGA	GAA	AGT	960
Thr	Asp	Pro	Ile	Gly	Phe	Val	His	Arg	Ser	Ser	Leu	Arg	Gly	Glu	Ser	
305					310					315					320	
TGG	TTT	AGC	TTT	GTT	AAT	AGA	GCT	AAT	TTC	TCA	GAT	TTA	GAA	AAT	GCA	1008
Trp	Phe	Ser	Phe	Val	Asn	Arg	Ala	Asn	Phe	Ser	Asp	Leu	Glu	Asn	Ala	

325	330	335	
ATA CCT AAT CCT AGA CCG TCT TGG TTT TTA AAT AAT ATG ATT ATA TCT Ile Pro Asn Pro Arg Pro Ser Trp Phe Leu Asn Asn Met Ile Ile Ser 340 345 350			1056
ACT GGT TCA CTT ACA TTG CCG GTT AGC CCA AGT ACT GAT AGA GCG AGG Thr Gly Ser Leu Thr Leu Pro Val Ser Pro Ser Thr Asp Arg Ala Arg 355 360 365			1104
GTA TGG TAT GGA AGT CGA GAT CGA ATT TCC CCT GCT AAT TCA CAA TTT Val Trp Tyr Gly Ser Arg Asp Arg Ile Ser Pro Ala Asn Ser Gln Phe 370 375 380			1152
ATT ACT GAA CTA ATC TCT GGA CAA CAT ACG ACT GCT ACA CAA ACT ATT Ile Thr Glu Leu Ile Ser Gly Gln His Thr Thr Ala Thr Gln Thr Ile 385 390 395 400			1200
TTA GGG CGA AAT ATA TTT AGA GTA GAT TCT CAA GCT TGT AAT TTA AAT Leu Gly Arg Asn Ile Phe Arg Val Asp Ser Gln Ala Cys Asn Leu Asn 405 410 415			1248
GAT ACC ACA TAT GGA GTG AAT AGG GCG GTA TTT TAT CAT GAT GCG AGT Asp Thr Thr Tyr Gly Val Asn Arg Ala Val Phe Tyr His Asp Ala Ser 420 425 430			1296
GAA GGT TCT CAA AGA TCC GTG TAC GAG GGG TAT ATT CGA ACA ACT GGG Glu Gly Ser Gln Arg Ser Val Tyr Glu Gly Tyr Ile Arg Thr Thr Gly 435 440 445			1344
ATA GAT AAC CCT AGA GTT CAA AAT ATT AAC ACT TAT TTA CCT GGA GAA Ile Asp Asn Pro Arg Val Gln Asn Ile Asn Thr Tyr Leu Pro Gly Glu 450 455 460			1392
AAT TCA GAT ATC CCA ACT CCA GAA GAC TAT ACT CAT ATA TTA AGC ACA Asn Ser Asp Ile Pro Thr Pro Glu Asp Tyr Thr His Ile Leu Ser Thr 465 470 475 480			1440
ACA ATA AAT TTA ACA GGA GGA CTT AGA CAA GTA GCA TCT AAT CGC CGT Thr Ile Asn Leu Thr Gly Gly Leu Arg Gln Val Ala Ser Asn Arg Arg 485 490 495			1488
TCA TCT TTA GTA ATG TAT GGT TGG ACA CAT AAA AGT CTG GCT CGT AAC Ser Ser Leu Val Met Tyr Gly Trp Thr His Lys Ser Leu Ala Arg Asn 500 505 510			1536
AAT ACC ATT AAT CCA GAT AGA ATT ACA CAG ATA CCA TTG ACG AAG GTT Asn Thr Ile Asn Pro Asp Arg Ile Thr Gln Ile Pro Leu Thr Lys Val 515 520 525			1584
GAT ACC CGA GGC ACA GGT GTT TCT TAT GTG AAT GAT CCA GGA TTT ATA Asp Thr Arg Gly Thr Gly Val Ser Tyr Val Asn Asp Pro Gly Phe Ile 530 535 540			1632

002260-0999990

GGA GGA GCT CTA CTT CAA AGG ACT GAC CAT GGT TCG CTT GGA GTA TTG 1680
 Gly Gly Ala Leu Leu Gln Arg Thr Asp His Gly Ser Leu Gly Val Leu
 545 550 555 560

AGG GTC CAA TTT CCA CTT CAC TTA AGA CAA CAA TAT CGT ATT AGA GTC 1728
 Arg Val Gln Phe Pro Leu His Leu Arg Gln Tyr Arg Ile Arg Val
 565 570 575

CGT TAT GCT TCT ACA ACA AAT ATT CGA TTG AGT GTG AAT GGC AGT TTC 1776
 Arg Tyr Ala Ser Thr Thr Asn Ile Arg Leu Ser Val Asn Gly Ser Phe
 580 585 590

GGT ACT ATT TCT CAA AAT CTC CCT AGT ACA ATG AGA TTA GGA GAG GAT 1824
 Gly Thr Ile Ser Gln Asn Leu Pro Ser Thr Met Arg Leu Gly Glu Asp
 595 600 605

TTA AGA TAC GGA TCT TTT GCT ATA AGA GAG TTT AAT ACT TCT ATT AGA 1872
 Leu Arg Tyr Gly Ser Phe Ala Ile Arg Glu Phe Asn Thr Ser Ile Arg
 610 615 620

CCC ACT GCA AGT CCG GAC CAA ATT CGA TTG ACA ATA GAA CCA TCT TTT 1920
 Pro Thr Ala Ser Pro Asp Gln Ile Arg Leu Thr Ile Glu Pro Ser Phe
 625 630 635 640

ATT AGA CAA GAG GTC TAT GTA GAT AGA ATT GAG TTC ATT CCA GTT AAT 1968
 Ile Arg Gln Glu Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asn
 645 650 655

CCG ACG CGA GAG GCG AAA GAG GAT CTA GAA GCA GCA AAA AAA GCG GTG 2016
 Pro Thr Arg Glu Ala Lys Glu Asp Leu Glu Ala Ala Lys Lys Ala Val
 660 665 670

GCG AGC TTG TTT ACA CGC ACA AGG GAC GGA TTA CAA GTA AAT GTG AAA 2064
 Ala Ser Leu Phe Thr Arg Thr Arg Asp Gly Leu Gln Val Asn Val Lys
 675 680 685

GAT TAT CAA GTC GAT CAA GCG GCA AAT TTA GTG TCA TGC TTA TCA GAT 2112
 Asp Tyr Gln Val Asp Gln Ala Ala Asn Leu Val Ser Cys Leu Ser Asp
 690 695 700

GAA CAA TAT GGG TAT GAC AAA AAG ATG TTA TTG GAA GCG GTA CGT GCG 2160
 Glu Gln Tyr Gly Tyr Asp Lys Lys Met Leu Leu Glu Ala Val Arg Ala
 705 710 715 720

GCA AAA CGA CTT AGC CGA GAA CGC AAC TTA CTT CAG GAT CCA GAT TTT 2208
 Ala Lys Arg Leu Ser Arg Glu Arg Asn Leu Leu Gln Asp Pro Asp Phe
 725 730 735

AAT ACA ATC AAT AGT ACA GAA GAA AAT GGA TGG AAA GCA AGT AAC GGC 2256
 Asn Thr Ile Asn Ser Thr Glu Glu Asn Gly Trp Lys Ala Ser Asn Gly
 740 745 750

GTT ACT ATT AGT GAG GGC GGG CCA TTC TAT AAA GGC CGT GCA ATT CAG	2304
Val Thr Ile Ser Glu Gly Gly Pro Phe Tyr Lys Gly Arg Ala Ile Gln	
755 760 765	
CTA GCA AGT GCA CGA GAA AAT TAC CCA ACA TAC ATC TAT CAA AAA GTA	2352
Leu Ala Ser Ala Arg Glu Asn Tyr Pro Thr Tyr Ile Tyr Gln Lys Val	
770 775 780	
GAT GCA TCG GAG TTA AAG CCG TAT ACA CGT TAT AGA CTG GAT GGG TTC	2400
Asp Ala Ser Glu Leu Lys Pro Tyr Thr Arg Tyr Arg Leu Asp Gly Phe	
785 790 795 800	
GTG AAG AGT AGT CAA GAT TTA GAA ATT GAT CTC ATT CAC CAT CAT AAA	2448
Val Lys Ser Ser Gln Asp Leu Glu Ile Asp Leu Ile His His His Lys	
805 810 815	
GTC CAT CTT GTG AAA AAT GTA CCA GAT AAT TTA GTA TCT GAT ACT TAC	2496
Val His Leu Val Lys Asn Val Pro Asp Asn Leu Val Ser Asp Thr Tyr	
820 825 830	
CCA GAT GAT TCT TGT AGT GGA ATC AAT CGA TGT CAG GAA CAA CAG ATG	2544
Pro Asp Asp Ser Cys Ser Gly Ile Asn Arg Cys Gln Glu Gln Gln Met	
835 840 845	
GTA AAT GCG CAA CTG GAA ACA GAG CAT CAT CAT CCG ATG GAT TGC TGT	2592
Val Asn Ala Gln Leu Glu Thr Glu His His His Pro Met Asp Cys Cys	
850 855 860	
GAA GCA GCT CAA ACA CAT GAG TTT TCT TCC TAT ATT GAT ACA GGG GAT	2640
Glu Ala Ala Gln Thr His Glu Phe Ser Ser Tyr Ile Asp Thr Gly Asp	
865 870 875 880	
TTA AAT TCG AGT GTA GAC CAG GGA ATC TGG GCG ATC TTT AAA GTT CGA	2688
Leu Asn Ser Ser Val Asp Gln Gly Ile Trp Ala Ile Phe Lys Val Arg	
885 890 895	
ACA ACC GAT GGT TAT GCG ACG TTA GGA AAT CTT GAA TTG GTA GAG GTC	2736
Thr Thr Asp Gly Tyr Ala Thr Leu Gly Asn Leu Glu Leu Val Glu Val	
900 905 910	
GGA CCG TTA TCG GGT GAA TCT TTA GAA CGT GAA CAA AGG GAT AAT ACA	2784
Gly Pro Leu Ser Gly Glu Ser Leu Glu Arg Glu Gln Arg Asp Asn Thr	
915 920 925	
AAA TGG AGT GCA GAG CTA GGA AGA AAG CGT GCA GAA ACA GAT CGC GTG	2832
Lys Trp Ser Ala Glu Leu Gly Arg Lys Arg Ala Glu Thr Asp Arg Val	
930 935 940	
TAT CAA GAT GCC AAA CAA TCC ATC AAT CAT TTA TTT GTG GAT TAT CAA	2880
Tyr Gln Asp Ala Lys Gln Ser Ile Asn His Leu Phe Val Asp Tyr Gln	
945 950 955 960	
GAT CAA CAA TTA AAT CCA GAA ATA GGG ATG GCA GAT ATT ATG GAC GCT	2928

Asp Gln Gln Leu Asn Pro Glu Ile Gly Met Ala Asp Ile Met Asp Ala
 965 970 975

CAA AAT CTT GTC GCA TCA ATT TCA GAT GTA TAT AGC GAT GCC GTA CTG 2976
 Gln Asn Leu Val Ala Ser Ile Ser Asp Val Tyr Ser Asp Ala Val Leu
 980 985 990

CAA ATC CCT GGA ATT AAC TAT GAG ATT TAC ACA GAG CTG TCC AAT CGC 3024
 Gln Ile Pro Gly Ile Asn Tyr Glu Ile Tyr Thr Glu Leu Ser Asn Arg
 995 1000 1005

TTA CAA CAA GCA TCG TAT CTG TAT ACG TCT CGA AAT GCG GTG CAA AAT 3072
 Leu Gln Gln Ala Ser Tyr Leu Tyr Thr Ser Arg Asn Ala Val Gln Asn
 1010 1015 1020

GGG GAC TTT AAC AAC GGG CTA GAT AGC TGG AAT GCA ACA GCG GGT GCA 3120
 Gly Asp Phe Asn Asn Gly Leu Asp Ser Trp Asn Ala Thr Ala Gly Ala
 1025 1030 1035 1040

TCG GTA CAA CAG GAT GGC AAT ACG CAT TTC TTA GTT CTT TCT CAT TGG 3168
 Ser Val Gln Gln Asp Gly Asn Thr His Phe Leu Val Leu Ser His Trp
 1045 1050 1055

GAT GCA CAA GTT TCT CAA CAA TTT AGA GTG CAG CCG AAT TGT AAA TAT 3216
 Asp Ala Gln Val Ser Gln Gln Phe Arg Val Gln Pro Asn Cys Lys Tyr
 1060 1065 1070

GTA TTA CGT GTA ACA GCA GAG AAA GTA GGC GGC GGA GAC GGA TAC GTG 3264
 Val Leu Arg Val Thr Ala Glu Lys Val Gly Gly Gly Asp Gly Tyr Val
 1075 1080 1085

ACT ATC CGG GAT GAT GCT CAT CAT ACA GAA ACG CTT ACA TTT AAT GCA 3312
 Thr Ile Arg Asp Asp Ala His His Thr Glu Thr Leu Thr Phe Asn Ala
 1090 1095 1100

TGT GAT TAT GAT ATA AAT GGC ACG TAC GTG ACT GAT AAT ACG TAT CTA 3360
 Cys Asp Tyr Asp Ile Asn Gly Thr Tyr Val Thr Asp Asn Thr Tyr Leu
 1105 1110 1115 1120

ACA AAA GAA GTG GTA TTC CAT CCG GAG ACA CAA CAC ATG TGG GTA GAG 3408
 Thr Lys Glu Val Val Phe His Pro Glu Thr Gln His Met Trp Val Glu
 1125 1130 1135

GTA AAT GAA ACA GAA GGT GCA TTT CAT ATA GAT AGT ATT GAA TTC GTT 3456
 Val Asn Glu Thr Glu Gly Ala Phe His Ile Asp Ser Ile Glu Phe Val
 1140 1145 1150

GAA ACA GAA AAG 3468
 Glu Thr Glu Lys
 1155

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1156 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Asn Gln Asn Lys His Gly Ile Ile Gly Ala Ser Asn Cys Gly Cys
 1 5 10 15

Ala Ser Asp Asp Val Ala Lys Tyr Pro Leu Ala Asn Asn Pro Tyr Ser
 20 25 30

Ser Ala Leu Asn Leu Asn Ser Cys Gln Asn Ser Ser Ile Leu Asn Trp
 35 40 45

Ile Asn Ile Ile Gly Asp Ala Ala Lys Glu Ala Val Ser Ile Gly Thr
 50 55 60

Thr Ile Val Ser Leu Ile Thr Ala Pro Ser Leu Thr Gly Leu Ile Ser
 65 70 75 80

Ile Val Tyr Asp Leu Ile Gly Lys Val Leu Gly Gly Ser Ser Gly Gln
 85 90 95

Ser Ile Ser Asp Leu Ser Ile Cys Asp Leu Leu Ser Ile Ile Asp Leu
 100 105 110

Arg Val Ser Gln Ser Val Leu Asn Asp Gly Ile Ala Asp Phe Asn Gly
 115 120 125

Ser Val Leu Leu Tyr Arg Asn Tyr Leu Glu Ala Leu Asp Ser Trp Asn
 130 135 140

Lys Asn Pro Asn Ser Ala Ser Ala Glu Glu Leu Arg Thr Arg Phe Arg
 145 150 155 160

Ile Ala Asp Ser Glu Phe Asp Arg Ile Leu Thr Arg Gly Ser Leu Thr
 165 170 175

Asn Gly Gly Ser Leu Ala Arg Gln Asn Ala Gln Ile Leu Leu Leu Pro
 180 185 190

Ser Phe Ala Ser Ala Ala Phe Phe His Leu Leu Leu Leu Arg Asp Ala
 195 200 205

Thr Arg Tyr Gly Thr Asn Trp Gly Leu Tyr Asn Ala Thr Pro Phe Ile
 210 215 220

Asn Tyr Gln Ser Lys Leu Val Glu Leu Ile Glu Leu Tyr Thr Asp Tyr

225 230 235 240
 Cys Val His Trp Tyr Asn Arg Gly Phe Asn Glu Leu Arg Gln Arg Gly
 245 250 255
 Thr Ser Ala Thr Ala Trp Leu Glu Phe His Arg Tyr Arg Arg Glu Met
 260 265 270
 Thr Leu Met Val Leu Asp Ile Val Ala Ser Phe Ser Ser Leu Asp Ile
 275 280 285
 Thr Asn Tyr Pro Ile Glu Thr Asp Phe Gln Leu Ser Arg Val Ile Tyr
 290 295 300
 Thr Asp Pro Ile Gly Phe Val His Arg Ser Ser Leu Arg Gly Glu Ser
 305 310 315 320
 Trp Phe Ser Phe Val Asn Arg Ala Asn Phe Ser Asp Leu Glu Asn Ala
 325 330 335
 Ile Pro Asn Pro Arg Pro Ser Trp Phe Leu Asn Asn Met Ile Ile Ser
 340 345 350
 Thr Gly Ser Leu Thr Leu Pro Val Ser Pro Ser Thr Asp Arg Ala Arg
 355 360 365
 Val Trp Tyr Gly Ser Arg Asp Arg Ile Ser Pro Ala Asn Ser Gln Phe
 370 375 380
 Ile Thr Glu Leu Ile Ser Gly Gln His Thr Thr Ala Thr Gln Thr Ile
 385 390 395 400
 Leu Gly Arg Asn Ile Phe Arg Val Asp Ser Gln Ala Cys Asn Leu Asn
 405 410 415
 Asp Thr Thr Tyr Gly Val Asn Arg Ala Val Phe Tyr His Asp Ala Ser
 420 425 430
 Glu Gly Ser Gln Arg Ser Val Tyr Glu Gly Tyr Ile Arg Thr Thr Gly
 435 440 445
 Ile Asp Asn Pro Arg Val Gln Asn Ile Asn Thr Tyr Leu Pro Gly Glu
 450 455 460
 Asn Ser Asp Ile Pro Thr Pro Glu Asp Tyr Thr His Ile Leu Ser Thr
 465 470 475 480
 Thr Ile Asn Leu Thr Gly Gly Leu Arg Gln Val Ala Ser Asn Arg Arg
 485 490 495
 Ser Ser Leu Val Met Tyr Gly Trp Thr His Lys Ser Leu Ala Arg Asn
 500 505 510

Asn Thr Ile Asn Pro Asp Arg Ile Thr Gln Ile Pro Leu Thr Lys Val
 515 520 525
 Asp Thr Arg Gly Thr Gly Val Ser Tyr Val Asn Asp Pro Gly Phe Ile
 530 535 540
 Gly Gly Ala Leu Leu Gln Arg Thr Asp His Gly Ser Leu Gly Val Leu
 545 550 555 560
 Arg Val Gln Phe Pro Leu His Leu Arg Gln Gln Tyr Arg Ile Arg Val
 565 570 575
 Arg Tyr Ala Ser Thr Thr Asn Ile Arg Leu Ser Val Asn Gly Ser Phe
 580 585 590
 Gly Thr Ile Ser Gln Asn Leu Pro Ser Thr Met Arg Leu Gly Glu Asp
 595 600 605
 Leu Arg Tyr Gly Ser Phe Ala Ile Arg Glu Phe Asn Thr Ser Ile Arg
 610 615 620
 Pro Thr Ala Ser Pro Asp Gln Ile Arg Leu Thr Ile Glu Pro Ser Phe
 625 630 635 640
 Ile Arg Gln Glu Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asn
 645 650 655
 Pro Thr Arg Glu Ala Lys Glu Asp Leu Glu Ala Ala Lys Lys Ala Val
 660 665 670
 Ala Ser Leu Phe Thr Arg Thr Arg Asp Gly Leu Gln Val Asn Val Lys
 675 680 685
 Asp Tyr Gln Val Asp Gln Ala Ala Asn Leu Val Ser Cys Leu Ser Asp
 690 695 700
 Glu Gln Tyr Gly Tyr Asp Lys Lys Met Leu Leu Glu Ala Val Arg Ala
 705 710 715 720
 Ala Lys Arg Leu Ser Arg Glu Arg Asn Leu Leu Gln Asp Pro Asp Phe
 725 730 735
 Asn Thr Ile Asn Ser Thr Glu Glu Asn Gly Trp Lys Ala Ser Asn Gly
 740 745 750
 Val Thr Ile Ser Glu Gly Gly Pro Phe Tyr Lys Gly Arg Ala Ile Gln
 755 760 765
 Leu Ala Ser Ala Arg Glu Asn Tyr Pro Thr Tyr Ile Tyr Gln Lys Val
 770 775 780
 Asp Ala Ser Glu Leu Lys Pro Tyr Thr Arg Tyr Arg Leu Asp Gly Phe
 785 790 795 800

Val Lys Ser Ser Gln Asp Leu Glu Ile Asp Leu Ile His His His Lys
805 810 815

Val His Leu Val Lys Asn Val Pro Asp Asn Leu Val Ser Asp Thr Tyr
820 825 830

Pro Asp Asp Ser Cys Ser Gly Ile Asn Arg Cys Gln Glu Gln Gln Met
835 840 845

Val Asn Ala Gln Leu Glu Thr Glu His His His Pro Met Asp Cys Cys
850 855 860

Glu Ala Ala Gln Thr His Glu Phe Ser Ser Tyr Ile Asp Thr Gly Asp
865 870 875 880

Leu Asn Ser Ser Val Asp Gln Gly Ile Trp Ala Ile Phe Lys Val Arg
885 890 895

Thr Thr Asp Gly Tyr Ala Thr Leu Gly Asn Leu Glu Leu Val Glu Val
900 905 910

Gly Pro Leu Ser Gly Glu Ser Leu Glu Arg Glu Gln Arg Asp Asn Thr
915 920 925

Lys Trp Ser Ala Glu Leu Gly Arg Lys Arg Ala Glu Thr Asp Arg Val
930 935 940

Tyr Gln Asp Ala Lys Gln Ser Ile Asn His Leu Phe Val Asp Tyr Gln
945 950 955 960

Asp Gln Gln Leu Asn Pro Glu Ile Gly Met Ala Asp Ile Met Asp Ala
965 970 975

Gln Asn Leu Val Ala Ser Ile Ser Asp Val Tyr Ser Asp Ala Val Leu
980 985 990

Gln Ile Pro Gly Ile Asn Tyr Glu Ile Tyr Thr Glu Leu Ser Asn Arg
995 1000 1005

Leu Gln Gln Ala Ser Tyr Leu Tyr Thr Ser Arg Asn Ala Val Gln Asn
1010 1015 1020

Gly Asp Phe Asn Asn Gly Leu Asp Ser Trp Asn Ala Thr Ala Gly Ala
1025 1030 1035 1040

Ser Val Gln Gln Asp Gly Asn Thr His Phe Leu Val Leu Ser His Trp
1045 1050 1055

Asp Ala Gln Val Ser Gln Gln Phe Arg Val Gln Pro Asn Cys Lys Tyr
1060 1065 1070

Val Leu Arg Val Thr Ala Glu Lys Val Gly Gly Gly Asp Gly Tyr Val

1075

1080

1085

Thr Ile Arg Asp Asp Ala His His Thr Glu Thr Leu Thr Phe Asn Ala
 1090 1095 1100

Cys Asp Tyr Asp Ile Asn Gly Thr Tyr Val Thr Asp Asn Thr Tyr Leu
 1105 1110 1115 1120

Thr Lys Glu Val Val Phe His Pro Glu Thr Gln His Met Trp Val Glu
 1125 1130 1135

Val Asn Glu Thr Glu Gly Ala Phe His Ile Asp Ser Ile Glu Phe Val
 1140 1145 1150

Glu Thr Glu Lys
 1155

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATG AAT CAA AAT AAA CAC GGA ATT ATT GGC GCT TCC AAT TGT GGT TGT	48
Met Asn Gln Asn Lys His Gly Ile Ile Gly Ala Ser Asn Cys Gly Cys	
1 5 10 15	
GCA TCT GAT GAT GTT GCG AAA TAT CCT TTA GCC AAC AAT CCA TAT TCA	96
Ala Ser Asp Asp Val Ala Lys Tyr Pro Leu Ala Asn Asn Pro Tyr Ser	
20 25 30	
TCT GCT TTA AAT TTA AAT TCT TGT CAA AAT AGT AGT ATT CTC AAC TGG	144
Ser Ala Leu Asn Leu Asn Ser Cys Gln Asn Ser Ser Ile Leu Asn Trp	
35 40 45	
ATT AAC ATA ATA GGC GAT GCA GCA AAA GAA GCA GTA TCT ATT GGG ACA	192
Ile Asn Ile Ile Gly Asp Ala Ala Lys Glu Ala Val Ser Ile Gly Thr	
50 55 60	
ACC ATA GTC TCT CTT ATC ACA GCA CCT TCT CTT ACT GGA TTA ATT TCA	240

75

275	280	285	
ACT AAT TAC CCA ATA GAA ACA GAT TTT CAG TTG AGT AGG GTC ATT TAT			912
Thr Asn Tyr Pro Ile Glu Thr Asp Phe Gln Leu Ser Arg Val Ile Tyr			
290	295	300	
ACA GAT CCA ATT GGT TTT GTA CAT CGT AGT AGT CTT AGG GGA GAA AGT			960
Thr Asp Pro Ile Gly Phe Val His Arg Ser Ser Leu Arg Gly Glu Ser			
305	310	315	320
TGG TTT AGC TTT GTT AAT AGA GCT AAT TTC TCA GAT TTA GAA AAT GCA			1008
Trp Phe Ser Phe Val Asn Arg Ala Asn Phe Ser Asp Leu Glu Asn Ala			
325	330	335	
ATA CCT AAT CCT AGA CCG TCT TGG TTT TTA AAT AAT ATG ATT ATA TCT			1056
Ile Pro Asn Pro Arg Pro Ser Trp Phe Leu Asn Asn Met Ile Ile Ser			
340	345	350	
ACT GGT TCA CTT ACA TTG CCG GTT AGC CCA AGT ACT GAT AGA GCG AGG			1104
Thr Gly Ser Leu Thr Leu Pro Val Ser Pro Ser Thr Asp Arg Ala Arg			
355	360	365	
GTA TGG TAT GGA AGT CGA GAT CGA ATT TCC CCT GCT AAT TCA CAA TTT			1152
Val Trp Tyr Gly Ser Arg Asp Arg Ile Ser Pro Ala Asn Ser Gln Phe			
370	375	380	
ATT ACT GAA CTA ATC TCT GGA CAA CAT ACG ACT GCT ACA CAA ACT ATT			1200
Ile Thr Glu Leu Ile Ser Gly Gln His Thr Thr Ala Thr Gln Thr Ile			
385	390	395	400
TTA GGG CGA AAT ATA TTT AGA GTA GAT TCT CAA GCT TGT AAT TTA AAT			1248
Leu Gly Arg Asn Ile Phe Arg Val Asp Ser Gln Ala Cys Asn Leu Asn			
405	410	415	
GAT ACC ACA TAT GGA GTG AAT AGG GCG GTA TTT TAT CAT GAT GCG AGT			1296
Asp Thr Thr Tyr Gly Val Asn Arg Ala Val Phe Tyr His Asp Ala Ser			
420	425	430	
GAA GGT TCT CAA AGA TCC GTG TAC GAG GGG TAT ATT CGA ACA ACT GGG			1344
Glu Gly Ser Gln Arg Ser Val Tyr Glu Gly Tyr Ile Arg Thr Thr Gly			
435	440	445	
ATA GAT AAC CCT AGA GTT CAA AAT ATT AAC ACT TAT TTA CCT GGA GAA			1392
Ile Asp Asn Pro Arg Val Gln Asn Ile Asn Thr Tyr Leu Pro Gly Glu			
450	455	460	
AAT TCA GAT ATC CCA ACT CCA GAA GAC TAT ACT CAT ATA TTA AGC ACA			1440
Asn Ser Asp Ile Pro Thr Pro Glu Asp Tyr Thr His Ile Leu Ser Thr			
465	470	475	480
ACA ATA AAT TTA AGA GGA GGA CTT AGA CAA GTA GCA TCT AAT CGC CGT			1488
Thr Ile Asn Leu Thr Gly Gly Leu Arg Gln Val Ala Ser Asn Arg Arg			
485	490	495	

TCA	TCT	TTA	GTA	ATG	TAT	GGT	TGG	ACA	CAT	AAA	AGT	CTG	GCT	CGT	AAC	1536
Ser	Ser	Leu	Val	Met	Tyr	Gly	Trp	Thr	His	Lys	Ser	Leu	Ala	Arg	Asn	
		500					505					510				
AAT	ACC	ATT	AAT	CCA	GAT	AGA	ATT	ACA	CAG	ATA	CCT	TTA	GTG	AAA	GGA	1584
Asn	Thr	Ile	Asn	Pro	Asp	Arg	Ile	Thr	Gln	Ile	Pro	Leu	Val	Lys	Gly	
		515					520					525				
TTT	AGA	GTT	TGG	GGG	GGC	ACC	TCT	GTC	ATT	ACA	GGA	CCA	GGA	TTT	ACA	1632
Phe	Arg	Val	Trp	Gly	Gly	Thr	Ser	Val	Ile	Thr	Gly	Pro	Gly	Phe	Thr	
		530					535				540					
GGA	GGG	GAT	ATC	CTT	CGA	AGA	AAT	ACC	TTT	GGT	GAT	TTT	GTA	TCT	CTA	1680
Gly	Gly	Asp	Ile	Leu	Arg	Arg	Asn	Thr	Phe	Gly	Asp	Phe	Val	Ser	Leu	
545					550				555						560	
CAA	GTC	AAT	ATT	AAT	TCA	CCA	ATT	ACC	CAA	AGA	TAC	CGT	TTA	AGA	TTT	1728
Gln	Val	Asn	Ile	Asn	Ser	Pro	Ile	Thr	Gln	Arg	Tyr	Arg	Leu	Arg	Phe	
				565					570						575	
CGT	TAC	GCT	TCC	AGT	AGG	GAT	GCA	CGA	GTT	ATA	GTA	TTA	ACA	GGA	GCG	1776
Arg	Tyr	Ala	Ser	Ser	Arg	Asp	Ala	Arg	Val	Ile	Val	Leu	Thr	Gly	Ala	
			580					585					590			
GCA	TCC	ACA	GGA	GTG	GGA	GGC	CAA	GTT	AGT	GTA	AAT	ATG	CCT	CTT	CAG	1824
Ala	Ser	Thr	Gly	Val	Gly	Gly	Gln	Val	Ser	Val	Asn	Met	Pro	Leu	Gln	
		595					600					605				
AAA	ACT	ATG	GAA	ATA	GGG	GAG	AAC	TTA	ACA	TCT	AGA	ACA	TTT	AGA	TAT	1872
Lys	Thr	Met	Glu	Ile	Gly	Glu	Asn	Leu	Thr	Ser	Arg	Thr	Phe	Arg	Tyr	
		610				615					620					
ACC	GAT	TTT	AGT	AAT	CCT	TTT	TCA	TTT	AGA	GCT	AAT	CCA	GAT	ATA	ATT	1920
Thr	Asp	Phe	Ser	Asn	Pro	Phe	Ser	Phe	Arg	Ala	Asn	Pro	Asp	Ile	Ile	
625					630				635					640		
GGG	ATA	AGT	GAA	CAA	CCT	CTA	TTT	GGT	GCA	GGT	TCT	ATT	AGT	AGC	GGT	1968
Gly	Ile	Ser	Glu	Gln	Pro	Leu	Phe	Gly	Ala	Gly	Ser	Ile	Ser	Ser	Gly	
				645				650					655			
GAA	CTT	TAT	ATA	GAT	AAA	ATT	GAA	ATT	ATT	CTA	GCA	GAT	GCA	ACA	TTT	2016
Glu	Leu	Tyr	Ile	Asp	Lys	Ile	Glu	Ile	Ile	Leu	Ala	Asp	Ala	Thr	Phe	
			660				665					670				
GAA	GCA	GAA	TCT	GAT	TTA	GAA	AGA	GCA	CAA	AAG	GCG	GTG	AAT	GCC	CTG	2064
Glu	Ala	Glu	Ser	Asp	Leu	Glu	Arg	Ala	Gln	Lys	Ala	Val	Asn	Ala	Leu	
		675					680					685				
TTT	ACT	TCT	TCC	AAT	CAA	ATC	GGG	TTA	AAA	ACC	GAT	GTG	ACG	GAT	TAT	2112
Phe	Thr	Ser	Ser	Asn	Gln	Ile	Gly	Leu	Lys	Thr	Asp	Val	Thr	Asp	Tyr	
		690				695					700					

CAT ATT GAT CAA GTA TCC AAT TTA GTG GAT TGT TTA TCA GAT GAA TTT	2160
His Ile Asp Gln Val Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe	
705 710 715 720	
TGT CTG GAT GAA AAG CGA GAA TTG TCC GAG AAA GTC AAA CAT GCG AAG	2208
Cys Leu Asp Glu Lys Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys	
725 730 735	
CGA CTC AGT GAT GAG CGG AAT TTA CTT CAA GAT CCA AAC TTC AGA GGG	2256
Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly	
740 745 750	
ATC AAT AGA CAA CCA GAC CGT GGC TGG AGA GGA AGT ACA GAT ATT ACC	2304
Ile Asn Arg Gln Pro Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr	
755 760 765	
ATC CAA GGA GGA GAT GAC GTA TTC AAA GAG AAT TAC GTC ACA CTA CCG	2352
Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro	
770 775 780	
GGT ACC GTT GAT GAG TGC TAT CCA ACG TAT TTA TAT CAG AAA ATA GAT	2400
Gly Thr Val Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp	
785 790 795 800	
GAG TCG AAA TTA AAA GCT TAT ACC CGT TAT GAA TTA AGA GGG TAT ATC	2448
Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile	
805 810 815	
GAA GAT AGT CAA GAC TTA GAA ATC TAT TTG ATC CGT TAC AAT GCA AAA	2496
Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys	
820 825 830	
CAC GAA ATA GTA AAT GTG CCA GGC ACG GGT TCC TTA TGG CCG CTT TCA	2544
His Glu Ile Val Asn Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser	
835 840 845	
GCC CAA AGT CCA ATC GGA AAG TGT GGA GAA CCG AAT CGA TGC GCG CCA	2592
Ala Gln Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro	
850 855 860	
CAC CTT GAA TGG AAT CCT GAT CTA GAT TGT TCC TGC AGA GAC GGG GAA	2640
His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu	
865 870 875 880	
AAA TGT GCA CAT CAT TCC CAT CAT TTC ACC TTG GAT ATT GAT GTT GGA	2688
Lys Cys Ala His His Ser His His Phe Thr Leu Asp Ile Asp Val Gly	
885 890 895	
TGT ACA GAC TTA AAT GAG GAC TTA GGT GTA TGG GTG ATA TTC AAG ATT	2736
Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile	
900 905 910	
AAG ACG CAA GAT GGC CAT GCA AGA CTA GGG AAT CTA GAG TTT CTC GAA	2784

Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu
 915 920 925

GAG AAA CCA TTA TTA GGG GAA GCA CTA GCT CGT GTG AAA AGA GCG GAG 2832
 Glu Lys Pro Leu Leu Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu
 930 935 940

AAG AAG TGG AGA GAC AAA CGA GAG AAA CTG CAG TTG GAA ACA AAT ATT 2880
 Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile
 945 950 955 960

GTT TAT AAA GAG GCA AAA GAA TCT GTA GAT GCT TTA TTT GTA AAC TCT 2928
 Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser
 965 970 975

CAA TAT GAT AGA TTA CAA GTG GAT ACG AAC ATC GCG ATG ATT CAT GCG 2976
 Gln Tyr Asp Arg Leu Gln Val Asp Thr Asn Ile Ala Met Ile His Ala
 980 985 990

GCA GAT AAA CGC GTT CAT AGA ATC CGG GAA GCG TAT CTG CCA GAG TTG 3024
 Ala Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu
 995 1000 1005

TCT GTG ATT CCA GGT GTC AAT GCG GCC ATT TTC GAA GAA TTA GAG GGA 3072
 Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly
 1010 1015 1020

CGT ATT TTT ACA GCG TAT TCC TTA TAT GAT GCG AGA AAT GTC ATT AAA 3120
 Arg Ile Phe Thr Ala Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys
 1025 1030 1035 1040

AAT GGC GAT TTC AAT AAT GGC TTA TTA TGC TGG AAC GTG AAA GGT CAT 3168
 Asn Gly Asp Phe Asn Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His
 1045 1050 1055

GTA GAT GTA GAA GAG CAA AAC AAC CAC CGT TCG GTC CTT GTT ATC CCA 3216
 Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu Val Ile Pro
 1060 1065 1070

GAA TGG GAG GCA GAA GTG TCA CAA GAG GTT CGT GTC TGT CCA GGT CGT 3264
 Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg
 1075 1080 1085

GGC TAT ATC CTT CGT GTC ACA GCA TAT AAA GAG GGA TAT GGA GAG GGC 3312
 Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly
 1090 1095 1100

TGC GTA ACG ATC CAT GAG ATC GAA GAC AAT ACA GAC GAA CTG AAA TTC 3360
 Cys Val Thr Ile His Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe
 1105 1110 1115 1120

AGC AAC TGT GTA GAA GAG GAA GTA TAT CCA AAC AAC ACA GTA ACG TGT 3408
 Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys

1125 1130 1135

AAT AAT TAT ACT GGG ACT CAA GAA GAA TAT GAG GGT ACG TAC ACT TCT 3456
 Asn Asn Tyr Thr Gly Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser
 1140 1145 1150

CGT AAT CAA GGA TAT GAC GAA GCC TAT GGT AAT AAC CCT TCC GTA CCA 3504
 Arg Asn Gln Gly Tyr Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro
 1155 1160 1165

GCT GAT TAC GCT TCA GTC TAT GAA GAA AAA TCG TAT ACA GAT GGA CGA 3552
 Ala Asp Tyr Ala Ser Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg
 1170 1175 1180

AGA GAG AAT CCT TGT GAA TCT AAC AGA GGC TAT GGG GAT TAC ACA CCA 3600
 Arg Glu Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro
 1185 1190 1195 1200

CTA CCG GCT GGT TAT GTA ACA AAG GAT TTA GAG TAC TTC CCA GAG ACC 3648
 Leu Pro Ala Gly Tyr Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr
 1205 1210 1215

GAT AAG GTA TGG ATT GAG ATC GGA GAA ACA GAA GGA ACA TTC ATC GTG 3696
 Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val
 1220 1225 1230

GAT AGC GTG GAA TTA CTC CTT ATG GAG GAA 3726
 Asp Ser Val Glu Leu Leu Leu Met Glu Glu
 1235 1240

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1242 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Asn Gln Asn Lys His Gly Ile Ile Gly Ala Ser Asn Cys Gly Cys
 1 5 10 15

Ala Ser Asp Asp Val Ala Lys Tyr Pro Leu Ala Asn Asn Pro Tyr Ser
 20 25 30

Ser Ala Leu Asn Leu Asn Ser Cys Gln Asn Ser Ser Ile Leu Asn Trp
 35 40 45

Ile Asn Ile Ile Gly Asp Ala Ala Lys Glu Ala Val Ser Ile Gly Thr
 50 55 60

Thr Ile Val Ser Leu Ile Thr Ala Pro Ser Leu Thr Gly Leu Ile Ser
 65 70 75 80
 Ile Val Tyr Asp Leu Ile Gly Lys Val Leu Gly Gly Ser Ser Gly Gln
 85 90 95
 Ser Ile Ser Asp Leu Ser Ile Cys Asp Leu Leu Ser Ile Ile Asp Leu
 100 105 110
 Arg Val Ser Gln Ser Val Leu Asn Asp Gly Ile Ala Asp Phe Asn Gly
 115 120 125
 Ser Val Leu Leu Tyr Arg Asn Tyr Leu Glu Ala Leu Asp Ser Trp Asn
 130 135 140
 Lys Asn Pro Asn Ser Ala Ser Ala Glu Glu Leu Arg Thr Arg Phe Arg
 145 150 155 160
 Ile Ala Asp Ser Glu Phe Asp Arg Ile Leu Thr Arg Gly Ser Leu Thr
 165 170 175
 Asn Gly Gly Ser Leu Ala Arg Gln Asn Ala Gln Ile Leu Leu Leu Pro
 180 185 190
 Ser Phe Ala Ser Ala Ala Phe Phe His Leu Leu Leu Leu Arg Asp Ala
 195 200 205
 Thr Arg Tyr Gly Thr Asn Trp Gly Leu Tyr Asn Ala Thr Pro Phe Ile
 210 215 220
 Asn Tyr Gln Ser Lys Leu Val Glu Leu Ile Glu Leu Tyr Thr Asp Tyr
 225 230 235 240
 Cys Val His Trp Tyr Asn Arg Gly Phe Asn Glu Leu Arg Gln Arg Gly
 245 250 255
 Thr Ser Ala Thr Ala Trp Leu Glu Phe His Arg Tyr Arg Arg Glu Met
 260 265 270
 Thr Leu Met Val Leu Asp Ile Val Ala Ser Phe Ser Ser Leu Asp Ile
 275 280 285
 Thr Asn Tyr Pro Ile Glu Thr Asp Phe Gln Leu Ser Arg Val Ile Tyr
 290 295 300
 Thr Asp Pro Ile Gly Phe Val His Arg Ser Ser Leu Arg Gly Glu Ser
 305 310 315 320
 Trp Phe Ser Phe Val Asn Arg Ala Asn Phe Ser Asp Leu Glu Asn Ala
 325 330 335
 Ile Pro Asn Pro Arg Pro Ser Trp Phe Leu Asn Asn Met Ile Ile Ser

82

Thr Asp Phe Ser Asn Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile
 625 630 635 640
 Gly Ile Ser Glu Gln Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly
 645 650 655
 Glu Leu Tyr Ile Asp Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe
 660 665 670
 Glu Ala Glu Ser Asp Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu
 675 680 685
 Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr
 690 695 700
 His Ile Asp Gln Val Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe
 705 710 715 720
 Cys Leu Asp Glu Lys Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys
 725 730 735
 Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly
 740 745 750
 Ile Asn Arg Gln Pro Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr
 755 760 765
 Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro
 770 775 780
 Gly Thr Val Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp
 785 790 795 800
 Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile
 805 810 815
 Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys
 820 825 830
 His Glu Ile Val Asn Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser
 835 840 845
 Ala Gln Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro
 850 855 860
 His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu
 865 870 875 880
 Lys Cys Ala His His Ser His His Phe Thr Leu Asp Ile Asp Val Gly
 885 890 895
 Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile
 900 905 910

Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu
915 920 925

Glu Lys Pro Leu Leu Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu
930 935 940

Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile
945 950 955 960

Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser
965 970 975

Gln Tyr Asp Arg Leu Gln Val Asp Thr Asn Ile Ala Met Ile His Ala
980 985 990

Ala Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu
995 1000 1005

Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly
1010 1015 1020

Arg Ile Phe Thr Ala Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys
1025 1030 1035 1040

Asn Gly Asp Phe Asn Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His
1045 1050 1055

Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu Val Ile Pro
1060 1065 1070

Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg
1075 1080 1085

Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly
1090 1095 1100

Cys Val Thr Ile His Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe
1105 1110 1115 1120

Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys
1125 1130 1135

Asn Asn Tyr Thr Gly Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser
1140 1145 1150

Arg Asn Gln Gly Tyr Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro
1155 1160 1165

Ala Asp Tyr Ala Ser Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg
1170 1175 1180

Arg Glu Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro

1185 1190 1195 1200

Leu Pro Ala Gly Tyr Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr
 1205 1210 1215

Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val
 1220 1225 1230

Asp Ser Val Glu Leu Leu Leu Met Glu Glu
 1235 1240

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "BglII site downstream of translation termination codon of CryIC."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATAAGATCTG TT

12

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCTAGCCATG GATCAAAATA AACACGGAAT TATTG

35

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTGGTCAGAT CTTTGAAGTA GAGCTCC

· 27

[illegible]